

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
 Run on: March 1, 2004, 16:36:28 ; Search time 54 Seconds  
 (without alignments)  
 596.489 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608  
 Sequence: 1 MARGSLRRLRLNLVGLWLA.....LSGFLVWRRCRERSSPPPX 114

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

- 1: geneseqP1980s:\*
- 2: geneseqP1990s:\*
- 3: geneseqP2000s:\*
- 4: geneseqP2001s:\*
- 5: geneseqP2002s:\*
- 6: geneseqP2003as:\*
- 7: geneseqP2003bs:\*
- 8: geneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	607	99.8	114	2	AAW73409	Aaw73409 Human sec
2	571	93.9	129	2	AAW88506	Aaw88506 Human liv
3	571	93.9	129	3	AY57940	Aay57940 Human tra
4	571	93.9	129	4	AAU03498	Aau03498 Human TWE
5	571	93.9	129	5	ABP61512	Abp61512 Human NF-
6	571	93.9	129	5	AAU79827	Aau79827 Human typ
7	571	93.9	129	6	ADA56889	Ada56889 Human sec
8	571	93.9	129	6	ABU56716	Abu56716 Lung canc
9	571	93.9	129	7	ADC74112	Adc74112 Human sec
10	571	93.9	129	7	ADD37867	Add37867 Human sec
11	571	93.9	129	7	ADD89033	Add89033 TAT274. 1
12	450	74.0	129	5	AAU79828	Aau79828 Mouse typ
13	433	71.2	309	4	AAU03500	Aau03500 Human TWE
14	274.5	45.1	112	3	AYY91463	Aay91463 Human sec
15	274.5	45.1	112	6	ADA57390	Ada57390 Human sec
16	274.5	45.1	112	7	ADC74462	Adc74462 Human sec
17	274.5	45.1	112	7	ADD38025	Add38025 Human sec
18	274.5	45.1	155	3	AYY91604	Aay91604 Human sec
19	274.5	45.1	155	6	ADA57391	Ada57391 Human sec
20	274.5	45.1	155	7	ADCT74463	Adct74463 Human sec
21	274.5	45.1	155	7	ADD38026	Add38026 Human sec
22	274.5	45.1	156	3	AYY91552	Aay91552 Human sec
23	191	31.4	32	6	ADA49370	Ada49370 Human En1
24	97.5	16.0	171	7	ADB90668	Adb90668 TALL-1R g
25	97.5	16.0	171	7	ADB90665	Adb90665 TALL-1R g

26	97.5	16.0	185	7	ADB90663	Adb90663 TALL-1R g
27	97	16.0	170	7	ADB90667	Adb90667 TALL-1R g
28	96.5	15.9	186	7	ADB90675	Adb90675 TALL-1R P
29	94.5	15.5	185	5	AAE22269	Aae22269 Human BAF
30	92.5	15.2	185	5	AAE22267	Aae22267 Human BAF
31	92.5	15.2	185	5	AAE22266	Aae22266 Human BAF
32	91.5	15.0	185	5	AAE22270	Aae22270 Human BAF
33	91.5	15.0	185	5	AAE22271	Aae22271 Human BAF
34	89.5	14.7	185	5	AAE22268	Aae22268 Human BAF
35	88.5	14.6	185	5	AAE22242	Aae22242 Human mat
36	88.5	14.6	1307	7	AAE39974	Aae39974 Human CRU
37	88.5	14.6	1307	7	ABP70118	Abp70118 Human NOV
38	88.5	14.6	1388	5	ABP70117	Abp70117 Human BRO
39	87.5	14.4	185	7	ABRB2287	Abb81483 Human Ztn
40	87	14.3	184	5	ABB81483	Aab81483 Human Ztn
41	87	14.3	184	6	AAE35227	Aae35227 Human BAF
42	87	14.3	184	6	ADA49363	Ada49363 Human aci
43	87	14.3	184	6	ABR61767	Abr61767 Human PRO
44	87	14.3	266	5	AAE22243	Aae22243 Human JST

#### ALIGNMENTS

RESULT 1						
ID	AAW73409	standard;	protein;	114 AA.		
XX	AAW73409;					
AC						
XX		DT 19-FEB-1999 (first entry)				
XX						
DE		Human secreted protein encoded by Gene No. 13.				
XX						
Secreted protein; human; protein therapy; gene therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disease; foetal deficiency; leukaemia; hepatic disease; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; immune system disorder; Alzheimers; schizophrenia; prostate disease; autoimmune disorder; AIDS.						
XX						
XX		Homo sapiens.				
XX						
Key						
FT						
FT		Location/Qualifiers				
FT						
XX						
PN	W09854206-A1.					
XX						
PD	03-DEC-1998.					
XX						
PF	28-MAY-1998;					
XX						
PR	30-MAY-1997;					
XX						
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	30-MAY-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PR	29-AUG-1997;					
PA	(HUMA-) HUMAN GENOME SCI INC.					
XX						
PI	Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;					
PI	Ni J, Feng P;					
DR	WPI; 1999-070209/06.					
DR	N-PSDB; AAV08823.					
XX	New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders					

PT or blood disorders.  
 XX Claim 11; Page 153; 188pp; English.  
 PS This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 129 AA;

XX Sequence 129 AA;

XX Sequence 129 AA;

CC This is the amino acid sequence of a transmembrane protein encoded by a human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAV84359-76) coding for 18 transmembrane proteins (see AAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large -scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines

XX

SQ

Sequence 129 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-55;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Qy 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLILWPLIGGALSLTFVGLLSGFLVWRRCRRERSSSPPP 113

XX Sequence 114 AA;

RESULT 2  
 ID AAW88506 Standard; protein: 129 AA.  
 XX AAW88506;  
 AC AAW88506;  
 XX DT 30-MAR-1999 (first entry)  
 DE Human liver clone HP10432-encoded membrane protein.  
 XX Transmembrane protein; HP10432; human; liver.  
 XX OS Homo sapiens.  
 XX PN WO9855508-A2.  
 XX PD 10-DEC-1998.  
 XX PP 03-JUN-1998; 98WO-JP002445.  
 XX PR 03-JUN-1997; 97JP-00144948.  
 XX PA (SAGA ) SAGAMI CHEM RES CENTRE.  
 PA (PROT-) PROTEGENE INC.  
 XX PI Kato S, Sekine S, Yamaguchi T;  
 XX DR WPI; 1999-045730/04.  
 DR N-PSDB; AAV84374.  
 XX New human proteins containing transmembrane domains and their encoding PT sequences - useful in the preparation of antibodies and large-scale PT protein production, gene diagnosis, and gene therapy.  
 XX PS Claim 1; Page 163; 229pp; English.  
 XX CC AAZ5669B to AAZ56776 encode AAY57877 to AAY57955 which represent human

CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The  
 CC transmembrane protein have immunospecific, antiproliferative and  
 CC neuroprotective activities. The human transmembrane proteins,  
 CC polynucleotides encoding them and other compositions and methods from the  
 CC present invention, can be used for the diagnosis, treatment or prevention  
 CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,  
 CC developmental and cell proliferative disorders. The HTMPN's can be used  
 CC to treat or prevent disorders associated with a decreased expression or  
 CC activity of HTMPN

XX Sequence 129 AA;

Query Match	93.9%	Score	571;	DB	3;	Length	129;
Best Local Similarity	94.7%	Pred. No.	8.4e-52;				
Matches	107;	Conservative	0;	Mismatches	6;	Indels	0;
Gaps	0;						

Db      1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60  
 Db      1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60

Qy      61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERSSPPP 113  
 Qy      61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113

Db      61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113

#### RESULT 4

ID AAU03498 standard; protein; 129 AA.

XX AAU03498;

AC AAU03498;

DT 26-SEP-2001 (first entry)

XX Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAK; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrothal fibroplasia;  
 KW rubesis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis.

OS Homo sapiens.

XX Key

FT Domain

FT      1..78 /note= "Extracellular domain"

FT Peptide

FT      1..27 /note= "Signal peptide"

FT Protein

FT      28..129 /note= "Mature human TWEAKR protein"

FT Domain

FT      79..101 /note= "Transmembrane domain"

FT Domain

FT      102..129 /note= "Intracellular domain"

XX PN WO200145730-A2.

XX PD 28-JUN-2001.

XX PF 19-DEC-2000; 2000WO-US034755.

XX PR 20-DEC-1999; 99US-0172878P.

XX PR 10-MAY-2000; 2000US-0203347P.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Wiley SR;

XX PI Matbuda A, Honda G, Muramatsu S, Nagano Y;

DR WPI; 2001-417975/44.  
 DR N-PSDB; AAS03963.

XX Modulating angiogenesis in a mammal for treating diseases mediated by  
 PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or  
 PT peripheral tissue, by administering antagonist or agonist of TWEAK  
 PT receptor.

XX Example 1; Fig 1; 46pp; English.

XX The sequence represents the human TWEAK receptor (TWEAK) protein. The  
 CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and  
 CC induces angiogenesis. TWEAK may therefore be used to screen for and  
 CC develop TWEAK agonists and antagonists for the modulation of  
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.  
 CC The disorders mediated by angiogenesis include ocular disorders  
 CC characterised by ocular neovascularisation such as diabetic retinopathy,  
 CC neovascular glaucoma, retinopathy of prematurity,  
 CC retrothal fibroplasia, rubesis, uveitis, macular degeneration and  
 CC corneal graft neovascularisation, and inflammatory diseases such as  
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include  
 CC malignant and metastatic conditions such as sarcomas and carcinomas,  
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,  
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic  
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary  
 CC atherosclerosis, peripheral atherosclerosis and ischaemia

XX	Sequence 129 AA;	Score	571;	DB	4;	Length	129;	
CC	Query Match	93.9%;	Score	571;	DB	4;	Length	129;
CC	Best Local Similarity	94.7%;	Pred. No.	8.4e-52;				
CC	Matches	107;	Conservative	0;	Mismatches	6;	Indels	0;
CC	Gaps	0;						
Qy	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60	Db	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60					
Qy	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60	Db	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60					
Qy	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERSSPPP 113	Db	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113					
Qy	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113	Db	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113					
XX	Sequence 129 AA;	Score	571;	DB	4;	Length	129;	
XX	Query Match	93.9%;	Pred. No.	8.4e-52;				
XX	Best Local Similarity	94.7%;	Pred. No.	8.4e-52;				
XX	Matches	107;	Conservative	0;	Mismatches	6;	Indels	0;
XX	Gaps	0;						
Qy	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60	Db	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60					
Qy	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60	Db	1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCASCRARPH 60					
Qy	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERSSPPP 113	Db	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113					
Qy	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113	Db	61 SDFCLGCAAAPPAPFLWLPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113					

RESULT 5  
 ID ABP61512 standard; protein; 129 AA.

XX ABP61512

XX ABP61512 standard; protein; 129 AA.

XX ABP61512;

XX AC

XX DT 30-SEP-2002 (first entry)

XX DT

XX DE Human NF-kB activating protein SEQ ID NO 178.

XX KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;

KW immunomodulator; Cytostatic; antiinfective; osteopathic; nootropic;

KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;

KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX KW Homo sapiens.

XX OS

XX PN WO200253737-A1.

XX XX 11-JUL-2002.

XX PD 25-DEC-2001; 2001WO-JP011389.

XX PR 28-DEC-2000; 2000JP-00402288.

XX PR 26-MAR-2001; 2001JP-00088912.

XX PR 24-AUG-2001; 2001JP-00254018.

XX XX (ASAHI KASEI KOGYO KK.

XX PI

XX XX

DR WPI; 2002-593617/62.  
 DR N-PSDB; ABQ92000.  
 XX DR  
 PR NF-activating gene and expressed protein, applicable in  
 PT diagnosis and screening inhibitors or promoters to control excessive  
 PT activation or inhibition for treating e.g. inflammations, autoimmune  
 PT diseases and cancer.  
 XX PS Claim 4; Page 814-815; 841PP; Japanese.  
 XX The invention relates to a purified protein (I), comprising one of 90  
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
 CC the sequences but with some amino acids deleted, substituted or added and  
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
 CC inhibitors or promoters to control excessive activation or inhibition and  
 CC for treating e.g. inflammations, autoimmune diseases, cancers,  
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
 CC disorders  
 XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 5; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 XX QY 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 QY 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113  
 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERKFTTP 113  
 Db RESULT 7  
 ADA56889 standard; protein; 129 AA.  
 XX QY 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113  
 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERKFTTP 113  
 Db

RESULT 6  
 AAU79827 standard; protein; 129 AA.  
 XX AC AAU79827;  
 XX DT 15-JUL-2002 (First entry)  
 XX DE Human type 1 transmembrane protein Fn14.  
 XX Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
 XX tumour necrosis factor family; TNF family; TWEAK receptor;  
 XX myocardial ischaemic condition; myocardial infarction; wound healing;  
 XX burn healing; gastric ulcer; tissue transplantation;  
 XX organ transplantation; neovascularisation; vascular insufficiency;  
 XX cancer; inflammatory macular degeneration; diabetic retinopathy.  
 XX OS Homo sapiens.  
 XX PN WO200222166-A2.  
 XX PD 21-MAR-2002.  
 XX PF 12-SEP-2001; 2001WO-US028451.  
 XX PR 14-SEP-2000; 2000US-0232355P.  
 XX PA (BIOJ ) BIOPHARMA INC.  
 XX PI Browning J, Burkly L, Jakubowski A, Zheng T;  
 XX DR WPI; 2002-383103/41.

XX PT Methods of modulating angiogenesis and inhibiting tumor progression,  
 PT using TWEAK receptor agonists.  
 XX Disclosure; Fig 10A; 37PP; English.  
 XX DR  
 XX PT New human secreted polypeptides and polynucleotides, useful for  
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
 PT conditions, respiratory disorders, cancers, CNS disorders, or  
 PT neurodegenerative disorders.  
 XX

XX The invention describes methods of modulating angiogenesis and inhibiting  
 CC tumour progression using TWEAK (a novel member of the tumour necrosis  
 CC factor or TNF family) receptor agonists. Conditions which can be treated  
 CC using the agonists include myocardial ischaemic conditions (e.g.  
 CC myocardial infarction), wound healing and healing of  
 CC gastric ulcers), and tissue and organ transplantations to promote  
 CC neovascularisation, particularly in subjects suffering from vascular  
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
 CC subsequently neovascularisation is useful in treatment of cancer,  
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
 CC described in the invention  
 XX SQ Sequence 129 AA;  
 Query Match 93.9%; Score 571; DB 5; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 XX QY 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 QY 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113  
 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERKFTTP 113  
 Db RESULT 7  
 ADA56889 standard; protein; 129 AA.  
 XX QY 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113  
 61 SDFCLGCAAAPPAPERLLWPLGGALSLTFVLGLLSGFLVWRRCRRERKFTTP 113  
 Db  
 XX DT 20-NOV-2003 (first entry)  
 XX ID ADA56889  
 XX XX  
 XX AC ADA56889;  
 XX XX  
 XX DT  
 XX DE Human secreted protein #172.  
 XX XX  
 XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
 XX KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
 XX KW cardiovascular; antiarteriosclerotic; gene therapy;  
 XX KW human secreted protein; immune disorder; inflammation;  
 XX KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
 XX KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
 XX KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
 XX KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
 XX KW triple helix formation; antisense gene therapy; forensic biology.  
 XX OS Homo sapiens.  
 XX PN WO2002102994-A2.  
 XX PD 27-DEC-2002.  
 XX XX  
 XX PF 19-MAR-2002; 2002WO-US008278.  
 XX PR 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM;  
 XX DR WPI; 2003-167512/16.  
 XX N-PSDB; ADA55993.  
 XX DR  
 XX PT  
 PT  
 PT  
 PT  
 XX

PS Claim 13; SEQ ID NO 1079; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorder, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 129 AA;

xx Query Match 93.9%; Score 571; DB 6; Length 129;

xx Best Local Similarity 94.7%; Pred. No. 8.4e-52;

xx Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVLGWLALLRSVAGEQAPGTTAPCSRGSWSADLDKCMDCACSCRAPH 60  
Db 1 MARGSLRRLRLLVLGWLALLRSVAGEQAPGTTAPCSRGSWSADLDKCMDCACSCRAPH 60

Qy 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRERSSSPPP 113  
Db 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRREKFTTP 113

RESULT 8  
ABU56716 ID ABU56716 standard; protein; 129 AA.  
XX AC ABU56716;  
XX DT 02-APR-2003 (First entry)  
XX DE Lung cancer-associated polypeptide #309.

DE Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.  
XX WO2002B6443-A2.  
XX PD 31-OCT-2002.  
XX PF 18-APR-2002; 2002WO-US012476.  
XX PR 18-APR-2001; 2001US-0284770P.  
PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-0334370P.  
PR 12-APR-2002; 2002US-0372246P.  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX PI Aziz N, Murray R;  
XX DR WPI; 2003-093161/08.  
DR N-PSDB; ABX76445.  
XX Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

XX PS Claim 27; Page 429; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.

XX SQ Sequence 129 AA;

xx Query Match 93.9%; Score 571; DB 6; Length 129;

xx Best Local Similarity 94.7%; Pred. No. 8.4e-52;

xx Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVLGWLALLRSVAGEQAPGTTAPCSRGSWSADLDKCMDCACSCRAPH 60  
Db 1 MARGSLRRLRLLVLGWLALLRSVAGEQAPGTTAPCSRGSWSADLDKCMDCACSCRAPH 60

Qy 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRERSSSPPP 113  
Db 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRREKFTTP 113

Qy 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRREKFTTP 113  
Db 61 SDFCLGCAAAAPPAPERLLWPILGGALSLTFTVLGLSGFLVWRCCRREKFTTP 113

RESULT 9  
ADC74112 ID ADC74112 standard; protein; 129 AA.  
XX AC ADC74112;  
XX DT 01-JAN-2004 (First entry)  
XX DE Human Secreted protein - SEQ ID 745.  
XX KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide; fungicide; antiparasitic; antiarteriosclerotic; vulnary; cytostatic; haemopoietic; haematologic; anaemia; autoimmune disorder;  
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

KW human.  
 XX OS Homo sapiens.  
 XX PN WO2003038063-A2.  
 XX PD 14-NOV-2002.  
 XX 08-MAY-2003.  
 XX PF 19-MAR-2002; 2002WO-US008277.  
 XX PR 21-MAR-2001; 2001US-0277340P.  
 XX PR 19-JUL-2001; 2001US-0306171P.  
 XX PR 13-NOV-2001; 2001US-0331287P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM;  
 XX DR WPI; 2003-140218/13.  
 XX PT New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, or related immediate hypersensitivity disorders.  
 XX PS Claim 1; SEQ ID NO 349; 1323pp; English.  
 XX CC The present invention relates to an isolated polypeptide or human secreted protein. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders. The polypeptide is also useful for identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or decreases the activity of the polypeptide. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating inflammatory disorders, neoplastic diseases, wound healing and disorders of epithelial cell proliferation, cardiovascular disorders, blood-related disorders, immune disorders, endocrine disorders, or gastrointestinal disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The present sequence represents a human secreted protein.  
 XX SQ Sequence 129 AA;  
 XX Query Match 93.9%; Score 571; DB 7; Length 129;  
 XX Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 XX Matches 0; Mismatches 6; Indels 0; Gaps 0;  
 XX Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 XX Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 DB 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 QY 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRRERSSSPPP 113  
 DB 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRREREKFTTP 113  
 QY 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRREREKFTTP 113  
 DB 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRREREKFTTP 113  
 XX RESULT 10  
 ID ADD37867 standard; protein; 129 AA.  
 AC ADD37867;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE TAT274.  
 XX KW human secreted protein; Antiallergic; Immunosuppressive; Hemostatic.  
 KW Anti-HIV; Cytostatic; Cytostatic; tumour; tumour-associated antigenic target polypeptide; tumour; cancer.

XX OS Homo sapiens.  
 XX WO2003057160-A2.  
 XX PD 17-JUL-2003.  
 XX PF 30-DEC-2002; 2002WO-US041798.  
 XX PR 02-JAN-2002; 2002US-0345444P.  
 PR 25-JAN-2002; 2002US-0351885P.  
 PR 25-FEB-2002; 2002US-0360066P.  
 PR 05-MAR-2002; 2002US-0362004P.  
 PR 20-MAR-2002; 2002US-0366869P.  
 PR 21-MAR-2002; 2002US-0366284P.  
 PR 28-MAR-2002; 2002US-0368679P.  
 PR 19-AUG-2002; 2002US-0404809P.  
 PR 21-AUG-2002; 2002US-0405645P.  
 XX PA (GETH ) GENENTECH INC.  
 PI Frantz G, Hillian KJ, Phillips H, Polakis P, Smith V, Spencer SD;  
 PI Williams PM, Wu TD, Zhang Z;  
 XX DR 2003-569537/53.  
 DR N-PSDB; ADD89109.  
 XX New antibodies against tumor-associated antigenic target polypeptide,  
 PT useful for treating or diagnosing tumors or cancers in mammals, e.g.  
 PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell  
 PT carcinomas.  
 PS Claim 1; SEQ ID NO 37; 252pp; English.  
 XX The present invention relates to antibodies against tumour-associated  
 CC antigenic target polypeptide. The antibody is useful for treating or  
 CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung  
 CC cancer, breast cancer, colon cancer, ovarian cancer, prostate  
 CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The  
 CC present sequence represents a TAT polypeptide.  
 XX Sequence 129 AA:  
 Query Match 93.9%; Score 571; DB 7; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 RESULT 13  
 AAU03500  
 ID AAU03500 standard; protein; 309 AA.  
 XX DT 26-SEP-2001 (first entry)  
 XX DE Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.  
 XX KW TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrobulbar fibroplasia;  
 KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis; human IgG1; TWEAKR-FC; fusion protein.  
 XX OS Homo Sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1. .27  
 FT .note= "Signal peptide"  
 FT .309  
 Protein FT .note= "Mature human TWEAKR-FC fusion protein.  
 Specifically referred to in Claim 11"  
 Domain FT .79  
 /note= "From TWEAKR extracellular domain. Specifically referred to in Claims 4 and 10"  
 Region FT .81  
 /note= "From a BgIII cloning site"  
 Region FT .309  
 /note= "FC portion"  
 XX WO200145730-A2.  
 PN WO200145730-A2.  
 XX PD 28-JUN-2001.  
 XX PN WO20006698-A1.  
 XX PF 19-DEC-2000; 2000WO-US034755.  
 XX PR 20-DEC-1999; 99US-0172878P.  
 PR 10-MAY-2000; 2000US-0203347P.  
 XX PA (IMMUNEX CORP.  
 XX PI WILEY SR;  
 XX DR WPI; 2001-417975/44.  
 DR N-PSDB; AAS03965.  
 XX DR N-PSDB; AAA26358.  
 XX PS Claim 4; Page 45-46; 46pp; English.  
 XX The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKR) protein extracellular domain fused to an FC portion from human IgG1. This fusion protein, TWEAKR-FC, is used in the preparation of TWEAKR agonists and antagonists. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubesis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.  
 XX Sequence 309 AA;  
 XX Query Match 71.2%; Score 433; DB 4; Length 309;  
 Best Local Similarity 74.1%; Pred. No. 5.7e-37;  
 Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;  
 Qy 1 MARGSLRLRLVLLVIGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRLRLVLLVIGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPPFRILLWPLGGALSITFVLGLLSGGFLVWRRCRRERSPP 112  
 Db 61 SDFCLGCAAAPPAPPFRILLWPLGGALSITFVLGLLSGGFLVWRSCDKHTCPP 90  
 SQ Sequence 112 AA;

RESULT 14  
 AAY91463  
 ID AAY91463 standard; protein; 112 AA.  
 XX AC AAY91463;  
 XX DT 29-JUN-2000 (first entry)  
 XX DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.  
 XX KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
 antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;  
 osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;  
 antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;  
 immune disease; inflammation; blood disorder; tumour; chromosome 16.  
 XX KW OS Homo sapiens.  
 XX PN WO200006698-A1.  
 XX PD 10-FEB-2000.  
 XX PF 29-JUL-1999; 99WO-US017130.  
 XX PR 30-JUL-1998; 98US-0094657P.  
 PR 05-AUG-1998; 98US-0095486P.  
 PR 06-AUG-1998; 98US-0095454P.  
 PR 12-AUG-1998; 98US-0096319P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
 PI Lafleur D, Wei Y, Ni J, Florene KA, Young PE, Brewer LA;  
 PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
 XX DR 2000-195282/17.  
 XX DR N-PSDB; AAA26358.  
 XX PT New isolated human genes and the secreted polypeptides they encode,  
 useful for diagnosis and treatment of e.g. cancers, neurological  
 disorders, immune diseases, inflammation or blood disorders.  
 XX PT  
 PT  
 PT  
 XX DR  
 DR  
 XX PS Claim 11; Page 465; 634pp; English.  
 XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, development abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, spinal cord injuries, transplant rejection, arthritis, infections, AIDS, psoriasis, acne, schizophrenia, osteoporosis, diabetes, asthma, sepsis, gastrointestinal disorders, respiratory disorders, reproductive disorders, and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AA26345 and AAY91450 are sequences used in the exemplification of the present invention  
 XX SQ Sequence 112 AA;

Query Match 45.1%; Score 274.5; DB 3; Length 112;  
 Best Local Similarity 96.4%; Pred. No. 7.2e-21;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCA-SC 55  
   1 MARGSLRRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCSTSC 56

Db 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCSTSC 56

RESULT 15  
 ADA57390 standard; protein; 112 AA.

XX AC ADA57390;  
 XX 20-NOV-2003 (first entry)  
 XX DE Human secreted protein #172.  
 XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
 KW cardiovacular; antiarteriosclerotic; gene therapy;  
 KW human secreted protein; immune disorder; inflammation;  
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
 KW triple helix formation; antisense gene therapy; forensic biology.  
 XX OS Homo sapiens.  
 XX PN WO2002102994-A2.  
 XX PD 27-DEC-2002.  
 XX PF 19-MAR-2002; 2002WO-US008278.  
 XX PR 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM;  
 XX DR; 2003-167512/16.  
 XX DR; N-PSDB; ADA56496.

from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX SQ Sequence 112 AA;  
 Query Match 45.1%; Score 274.5; DB 6; Length 112;  
 Best Local Similarity 96.4%; Pred. No. 7.2e-21;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCSTSC 56

Search completed: March 1, 2004, 16:42:52  
 Job time : 77 secs

XX PS New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1582; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals

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OM protein - protein search, using SW model  
Run on: March 1, 2004, 16:41:53 ; Search time 23 Seconds  
(without alignments)  
255.885 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRLRLRLVGLWLA.....LSGFLVWRRRCRERESSPPPX 114  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Issued\_Patents\_AA:  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:  
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5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:  
7:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	607	99.8	114	4	US-09-690-454-59	Sequence 59, Appl
2	274.5	45.1	112	4	US-09-489-847-139	Sequence 139, App
3	274.5	45.1	155	4	US-09-489-847-284	Sequence 284, App
4	274.5	45.1	156	4	US-09-489-847-228	Sequence 228, App
5	96.5	15.9	248	4	US-09-252-991A-29249	Sequence 29249, A
6	88.5	14.6	400	4	US-09-252-991A-26145	Sequence 26145, A
7	87.5	14.4	631	4	US-09-252-991A-20063	Sequence 20063, A
8	83.5	13.7	152	4	US-09-252-991A-31619	Sequence 31619, A
9	80.5	13.2	249	4	US-09-252-991A-29850	Sequence 29850, A
10	76.5	12.6	250	4	US-09-322-409-31	Sequence 31, Appl
11	76.5	12.6	250	4	US-09-451-527-31	Sequence 31, Appl
12	76.5	12.6	276	4	US-09-322-409-26	Sequence 26, Appl
13	76.5	12.6	276	4	US-09-451-527-26	Sequence 26, Appl
14	75	12.3	334	4	US-09-252-991A-18795	Sequence 18795, A
15	74.5	12.3	305	4	US-09-252-991A-21147	Sequence 21147, A
16	73.5	12.1	187	4	US-09-199-637A-287	Sequence 287, App
17	73.5	12.1	187	4	US-09-252-991A-21454	Sequence 21454, A
18	72	11.8	1278	4	US-09-462-136-2	Sequence 2, Appl
19	72	11.8	3724	2	US-08-804-22C-10	Sequence 10, Appl
20	72	11.8	478	4	US-09-252-991A-18195	Sequence 4, Appl
21	71.5	11.6	402	4	US-09-252-991A-22078	Sequence 22078, A
22	70.5	11.6	402	4	US-09-462-136-2	Sequence 2, Appl
23	69.5	11.4	176	4	US-09-252-991A-25290	Sequence 25290, A
24	69	11.3	152	4	US-09-252-991A-24730	Sequence 24730, A
25	69	11.3	153	4	US-09-252-991A-20688	Sequence 20688, A
26	69	11.3	215	3	US-09-220-528-104	Sequence 104, App
27	69	11.3	511	4	US-09-252-991A-28223	Sequence 28223, A

28 68.5 11.3 127 4 US-09-489-039A-10884 Sequence 10884, A  
29 68.5 11.3 205 2 US-08-775-009-37 Sequence 37, Appl  
30 68.5 11.3 429 1 US-07-964-589-2 Sequence 2, Appl  
31 68.5 11.3 429 5 PCT-US93-02024-2 Sequence 2, Appl  
32 68 11.2 139 4 US-09-252-991A-17414 Sequence 17414, A  
33 68 11.2 144 4 US-09-252-991A-17313 Sequence 17313, A  
34 68 11.2 204 4 US-09-252-991A-29996 Sequence 29996, A  
35 68 11.2 282 4 US-09-252-991A-29124 Sequence 29124, A  
36 68 11.2 366 4 US-09-252-991A-31958 Sequence 31958, A  
37 68 11.2 775 4 US-09-252-991A-22300 Sequence 22300, A  
38 67.5 11.1 174 3 US-09-383-586-12 Sequence 12, Appl  
39 67.5 11.1 268 4 US-09-322-409-23 Sequence 23, Appl  
40 67.5 11.1 268 4 US-09-451-527-23 Sequence 23, Appl  
41 67.5 11.1 294 4 US-09-322-409-7 Sequence 7, Appl  
42 67.5 11.1 294 4 US-09-451-527-7 Sequence 7, Appl  
43 67.5 11.1 359 3 US-09-413-814-90 Sequence 90, Appl  
44 67.5 11.1 361 3 US-09-413-814-77 Sequence 77, Appl  
45 67 11.0 112 4 US-09-252-991A-21707 Sequence 21707, A

RESULT 1  
US-09-690-454-59

; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 3.2 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09-690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/044,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 99.8%; Score 607; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.5e-59;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLRLRLVGLWLA.....LSGFLVWRRRCRERESSPPPX 114  
Db 1 MARGSLRLRLRLVGLWLA.....LSGFLVWRRRCRERESSPPPX 114

Qy 61 SDFCLGCAAAPPAPERLWPILGALSLTFLVGLLSGFLYWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLWPILGALSLTFLVGLLSGFLYWRRCRRERSSSPPP 113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-07-30  
 ; EARLIER APPLICATION NUMBER: 60/095, 486  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/095, 455  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 139  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-489-847-139

Query Match 45.1%; Score 274.5; DB 4; Length 112;  
 Best Local Similarity 96.4%; Pred. No. 8.9e-23;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 Qy 1 MARGSLRRLRLVIGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVIGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCSTSC 56

RESULT 3  
 US-09-489-847-284  
 ; Sequence 284, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 284  
 ; LENGTH: 155  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-489-847-284

RESULT 4  
 US-09-489-847-228  
 ; Sequence 228, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-07-30  
 ; EARLIER APPLICATION NUMBER: 60/095, 486  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/095, 455  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/095, 455  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 228  
 ; LENGTH: 156  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (156)  
 ; OTHER INFORMATION: Xaa equals stop translation  
 ; US-09-489-847-228

Query Match 45.1%; Score 274.5; DB 4; Length 156;  
 Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 Qy 1 MARGSLRRLRLVIGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVIGLWLALLRSVAGEQAPGTAPCSRGGSSWSADL DKCMDCSTSC 56

RESULT 5  
 US-09-252-991A-29249  
 ; Sequence 29249, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196\_136  
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074, 788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094, 190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 29249  
 ; LENGTH: 248  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-489-847-284

US-09-252-991A-29249  
 Query Match 15.9%; Score 96.5; DB 4; Length 248;  
 Best Local Similarity 30.0%; Pred. No. 0.007;  
 Matches 27; Conservative 9; Mismatches 23; Indels 31; Gaps 4;  
 SEQ 18 WLALLRSVAGE-----QAPGTAPCSRGSG-----SWSADDL DKCM 50  
 DB 38 WCSSTRSGGAACRRCCRASSTAPCSRASPSSATAAPRTRTGSNCWAGAAPTCWSATT SCCR 97  
 RESULT 8  
 US-09-252-991A-31619  
 ; Sequence 31619, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196-136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 31619  
 ; LENGTH: 152  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-31619

Query Match 13.7%; Score 83.5; DB 4; Length 152;  
 Best Local Similarity 29.7%; Pred. No. 0.11;  
 Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;  
 SEQ ID NO 26145  
 PRIOR APPLICATION NUMBER: US/09/252,991A  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 26145  
 LENGTH: 400  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-26145

Query Match 14.6%; Score 88.5; DB 4; Length 400;  
 Best Local Similarity 38.3%; Pred. No. 0.091;  
 Matches 23; Conservative 4; Mismatches 30; Indels 3; Gaps 2;  
 SEQ 18 WLALLRSVAGEQAPGTAPCS--RGSSWSADLDKCMDCACSCRARPHSF DCLGCA-AAPPAP 74  
 DB 45 WSTAWRFPA TAAAGWPRCAWPMASNWATLSPRTSTASCRPMHRSACC AKSRPPAP 104  
 RESULT 9  
 US-09-252-991A-29850  
 ; Sequence 29850, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196-136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 29850  
 ; LENGTH: 249  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-29850

Query Match 13.2%; Score 80.5; DB 4; Length 249;  
 Best Local Similarity 30.5%; Pred. No. 0.4;  
 Matches 40; Conservative 8; Mismatches 32; Indels 51; Gaps 8;  
 SEQ 10 LRLLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC-----RA 57  
 DB 104 LRAVRLAAFCRLRAVAGARLVAAP--RGAGLAAPAQS--PAACSCANTS RSTFAPRLI 159  
 LENGTH: 631  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-20063

Query Match 14.4%; Score 87.5; DB 4; Length 631;  
 Best Local Similarity 32.6%; Pred. No. 0.2;  
 Matches 30; Conservative 6; Mismatches 43; Indels 13; Gaps 4;  
 SEQ 23 RSSVAGEQAPGTAPCSRGS-SWS-ADLDKCM--DCASCRARPHSF DCLGCAA APPAPFRLL 78  
 LENGTH: 631  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-20063

QY 58 RP-----HSDFCLGCA-AAPPAPFRLLW-----PILGGALSITFVLGLSGFLV 1.00 ; ORGANISM: Canis familiaris  
 Db 160 RPTFSPRRSRSCQAAASAAATPAPSATLWVLVKHRRMAAPI---SLSLT----- 205 ; SEQ ID NO: 451-527-31

Query Match 12.6%; Score 76.5; DB 4; Length 250;  
 Best Local Similarity 27.5%; Pred. No. 1.1;  
 Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

Qy 11 RLLVGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
 Db 49 RLVLQRMVRQLQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQOLAALKPWTIRRNFG 108

RESULT 10  
 Sequence 31, Application US/09322409  
 Patent No. 6471957  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Dreitz, Matthew J.  
 APPLICANT: Wonderling, Ramani S.  
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 FILE REFERENCE: IM-2-C1  
 CURRENT APPLICATION NUMBER: US/09/322,409  
 CURRENT FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 154  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 31  
 LENGTH: 250  
 TYPE: PRT  
 ORGANISM: Canis familiaris  
 US-09-322-409-31

Query Match 12.6%; Score 76.5; DB 4; Length 250;  
 Best Local Similarity 27.5%; Pred. No. 1.1;  
 Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

Qy 11 RLLVGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
 Db 49 RLVLQRMVRQLQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQOLAALKPWTIRRNFG 108

Qy 45 DLD-KCMDCASCRARPHSDFCLGCAA--APPAPFRLLWPILGGLSITFVLGLSGFLV 101  
 Db 109 CLELQCQPDSSSTLVPPRSPGALEATALPAPOAP-RLLLL---LPVALLMSTAACLHW 164

Qy 102 RRCCRERSSPP 112  
 Db 165 RRRRRRSPP 175

RESULT 12  
 Sequence 26, Application US/09322409  
 Patent No. 6471957  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Dreitz, Matthew J.  
 APPLICANT: Wonderling, Ramani S.  
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 FILE REFERENCE: IM-2-C1  
 CURRENT APPLICATION NUMBER: US/09/322,409  
 CURRENT FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 154  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 26  
 LENGTH: 276  
 TYPE: PRT  
 ORGANISM: Canis familiaris  
 US-09-322-409-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;  
 Best Local Similarity 27.5%; Pred. No. 1.2;  
 Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

Qy 11 RLLVGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
 Db 75 RLVLQRMVRQLQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQOLAALKPWTIRRNFG 134

Qy 45 DLD-KCMDCASCRARPHSDFCLGCAA--APPAPFRLLWPILGGLSITFVLGLSGFLV 101  
 Db 135 CLELQCQPDSSSTLVPPRSPGALEATALPAPOAP-RLLLL---LPVALLMSTAACLHW 190

Qy 102 RRCCRERSSPP 112  
 Db 191 RRRRRRSPP 201

RESULT 13  
 Sequence 26, Application US/09451527  
 Patent No. 6482403  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Dreitz, Matthew J.  
 APPLICANT: Wonderling, Ramani S.  
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 FILE REFERENCE: IM-2-C2  
 CURRENT APPLICATION NUMBER: US/09/451,527  
 CURRENT FILING DATE: 1999-12-01  
 EARLIER APPLICATION NUMBER: 09/322,409  
 EARLIER FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 174  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 31  
 LENGTH: 250  
 TYPE: PRT

CURRENT APPLICATION NUMBER: US/09/451,527  
 CURRENT FILING DATE: 1999-12-01  
 EARLIER APPLICATION NUMBER: 09/322,409  
 EARLIER FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 174  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 26  
 LENGTH: 276  
 TYPE: PRT  
 ORGANISM: Canis familiaris  
 US-09-451-527-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;  
 Best Local Similarity 27.5%; Pred. No. 1.2;  
 Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

Qy 11 RLLVGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
 Db 75 RLVLAQRMMVRILQAVAGGSMQILLEAVNTEIHFTFCAFQDTSQQLAAALKPWIIRRNFSG 134

Qy 45 DLD-KCMDCASCRARPHSDFCLGCAA-APPAPFRLLWPIGGALSITFVLGLLSGFLVW 101  
 Db 135 CLELQCQPDSTLVPPRSPGALEATALPAPQAP-RLLLL--LPVALIMSTAACLHW 190

Qy 102 RRCCRERSSPP 112  
 Db 191 RRRRRRRSPYP 201

RESULT 14  
 US-09-252-991A-18795  
 Sequence 18795, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO: 18795  
 LENGTH: 334  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-18795

Query Match 12.3%; Score 75; DB 4; Length 334;  
 Best Local Similarity 35.6%; Pred. No. 2.2;  
 Matches 26; Conservative 7; Mismatches 30; Indels 10; Gaps 4;

Qy 33 TAPCSRGSWSAIDLKCMDCASCRARPHSDFCLGCAAAPPAPER--LILWPILGGALSITF 90  
 Db 38 TTPTTSTARWSRPVP----APCLQAPAS--LLSTSTAPTATMADFLNALLAG-LALA 89

Qy 91 VLGLLSGFLVWRR 103  
 Db 90 VAGPLGSFVVWRR 102

RESULT 15  
 US-09-252-991A-21147  
 Sequence 21147, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

Sequence 7, Appli  
 Sequence 2, Appli  
 Sequence 6, Appli  
 Sequence 14, Appli  
 Sequence 17, Appli  
 Sequence 138, App  
 Sequence 140, App  
 Sequence 2, Appli  
 Sequence 60, Appli  
 Sequence 8962, Ap  
 Sequence 31, Appli  
 Sequence 31, Appli  
 Sequence 26, Appli  
 Sequence 26, Appli  
 Sequence 12251, A  
 Sequence 3127, Ap  
 Sequence 3845, Ap  
 Sequence 5911, Ap  
 Sequence 5912, Ap  
 Sequence 64, Appli  
 Sequence 12, Appli  
 Sequence 5165, Ap  
 Sequence 287, App  
 Sequence 11890, A  
 Sequence 6004, Ap  
 Sequence 5, Appli  
 Sequence 59, Appli  
 Sequence 2579, Ap  
 Sequence 3192, Ap  
 Sequence 2, Appli  
  
 14 US-10-251-947-7  
 14 US-10-251-947-2  
 14 US-10-251-947-6  
 14 US-10-251-947-14  
 14 US-10-303-685-17  
 15 US-10-093-463-138  
 15 US-10-093-463-140  
 15 US-10-093-463-140  
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 14 US-10-152-363A-60  
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 14 US-10-218-654-26  
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 15 US-10-085-198-64  
 15 US-10-434-156-12  
 15 US-10-369-493-5165  
 14 US-09-975-719-287  
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 14 US-10-208-731-2  
  
 16 97.5 16.0  
 17 97.5 16.0  
 18 97 16.0  
 19 96.5 15.9  
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 21 88.5 14.6  
 22 88.5 14.6  
 23 87 14.3  
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 25 79.5 13.1  
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 36 74 12.2  
 37 74 12.2  
 38 73.5 12.1  
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 171 14 185 14  
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 15 1388 15  
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 15 635 15  
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 15 548 15  
 15 768 15  
 10 187 10  
 14 409 14  
 9 242 9  
 10 365 10  
 14 365 14  
 15 391 15  
 15 257 15  
 14 1278 14

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.  
  
 I protein - protein search, using sw model  
  
 March 1, 2004, 16:43:58 ; Search time 33 Seconds  
 (without alignments)  
 729.439 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608  
 Sequence: 1 MARGSLRRLRLVGLWLA.....LSGFLVWRRCRRERSPPPX 114

Scoring table: BLOSUM62  
 GapOp 10.0 , GapExt 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Maximum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries  
 Published\_Applications\_AA:\*

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//cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep:*
//cgn2_6/ptodata/1/pubpaa/us08_NNEW_PUB.pep:*
//cgn2_6/ptodata/1/pubpaa/us09_NNEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	US-10-062-831-59	Sequence 59, Appl
2	607	99.8	114	US-10-062-599-59	Sequence 59, Appl
3	571	93.9	129	US-09-742-454A-4	Sequence 4, Appl
4	571	93.9	129	US-09-883-777-4	Sequence 4, Appl
5	571	93.9	129	US-10-024-298A-178	Sequence 178, App
6	571	93.9	129	US-10-042-211A-178	Sequence 178, App
7	571	93.9	129	US-10-331-496A-37	Sequence 37, Appl
8	571	93.9	129	US-10-295-027-444	Sequence 444, App
9	571	93.9	129	US-10-295-027-1305	Sequence 1305, Ap
10	450	74.0	129	US-09-742-454A-5	Sequence 5, Appl
11	450	74.0	129	US-09-883-777-5	Sequence 5, Appl
12	433	71.2	309	US-09-742-454A-7	Sequence 7, Appl
13	433	71.2	309	US-09-883-777-7	Sequence 7, Appl
14	379.5	62.4	300	US-09-883-777-9	Sequence 9, Appl
15	97.5	16.0	171	US-10-251-947-4	Sequence 4, Appl

RESULT 1  
US-10-062-831-59  
; Sequence 59, Application US/10062B31  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062, 831  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690, 454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044, 039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048, 093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048, 190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050, 935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048, 101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048, 356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056, 250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056, 296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056, 293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SITE  
 LOCATION: (114)  
 OTHER INFORMATION: Xaa equals stop translation  
 US-10-062-599-59

Query Match 99.8%; Score 607; DB 14; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113

---

RESULT 2  
 US-10-062-599-59  
 ; Sequence 59, Application US/10062599  
 Publication No. US20030195346A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Steven M. Ruben, et al.  
 ; TITLE OF INVENTION: 32 Human Secreted Proteins  
 FILE REFERENCE: PZ006P1  
 CURRENT APPLICATION NUMBER: US/10/062, 599  
 CURRENT FILING DATE: 2002-02-05  
 PRIOR APPLICATION NUMBER: 09/690, 454  
 PRIOR FILING DATE: 2000-10-18  
 PRIOR APPLICATION NUMBER: 09/189, 144  
 PRIOR FILING DATE: 1998-11-10  
 PRIOR APPLICATION NUMBER: 60/044, 039  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/048, 093  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/050, 935  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/048, 101  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/048, 356  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 250  
 PRIOR FILING DATE: August 29, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 296  
 PRIOR FILING DATE: August 29, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 293  
 PRIOR FILING DATE: August 29, 1997  
 NUMBER OF SEQ ID NOS: 229  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 59  
 LENGTH: 114  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (114)  
 OTHER INFORMATION: Xaa equals stop translation  
 US-10-062-599-59

Query Match 99.8%; Score 607; DB 14; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113

RESULT 3  
 US-09-742-454A-4  
 ; Sequence 4, Application US/09742454A  
 ; Patent No. US20020041876A1  
 GENERAL INFORMATION:  
 ; APPLICANT: WILEY, Steven R.  
 ; TITLE OF INVENTION: TWEAK Receptor  
 FILE REFERENCE: 2968-B  
 CURRENT APPLICATION NUMBER: US/09/742, 454A  
 CURRENT FILING DATE: 2000-12-19  
 PRIOR APPLICATION NUMBER: 60/172, 878  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: 60/203, 347  
 PRIOR FILING DATE: 2000-05-10  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 129  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-742-454A-4

Query Match 93.9%; Score 571; DB 9; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113

RESULT 4  
 US-09-883-777-4  
 ; Sequence 4, Application US/09883777  
 ; Patent No. US20020110853A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: TWEAK RECEPTOR  
 FILE REFERENCE: 2968-C  
 CURRENT APPLICATION NUMBER: US/09/883, 777  
 CURRENT FILING DATE: 2001-06-18  
 PRIOR APPLICATION NUMBER: US 60/172, 878  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: US 60/203, 347  
 PRIOR FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: PCT/US00/34755  
 PRIOR FILING DATE: 2000-12-19  
 PRIOR APPLICATION NUMBER: US 09/742, 454  
 PRIOR FILING DATE: 2000-12-19  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 4  
 LENGTH: 129  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-883-777-4

Query Match 93.9%; Score 571; DB 9; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60  
 Db 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLWRRCRRESSSSPPP 113

61 SDFCLGCAAAPPAPFLWPILGALSITFVLGLLSGFLLWRRREKFTTP 113

RESULT 5  
 US-10-024-298A-178  
 ; Sequence 178, Application US/10024298A  
 ; Publication No. US20030143540A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ASAHIBI KASEI KABUSHIKI KAISHA  
 ; APPLICANT: Akio MATSUDA  
 ; APPLICANT: Goichi HONDA  
 ; APPLICANT: Shuji MURAMATSU  
 ; APPLICANT: Yukiko NAGANO  
 ; TITLE OF INVENTION: NF-K B Activating Gene  
 ; FILE REFERENCE: 1254-0191P  
 ; CURRENT APPLICATION NUMBER: US/10/024,298A  
 ; CURRENT FILING DATE: 2003-04-08  
 ; PRIOR APPLICATION NUMBER: 60/314,385  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 60/278,641  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 60/258,315  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: JP254018/2001  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: JP0088912/2001  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: JP402288/2000  
 ; PRIOR FILING DATE: 2000-12-28  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 178  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 178  
 ; LENGTH: 129  
 ; Query Match 93.9%; Score 571; DB 14; Length 129;  
 ; Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 ; Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-042-211A-178  
 ; Sequence 178, Application US/10042211A  
 ; Publication No. US20030170719A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATSUDA, Akio et al.  
 ; TITLE OF INVENTION: NFkB Activating Gene  
 ; FILE REFERENCE: 1254-0192P  
 ; CURRENT APPLICATION NUMBER: US/10/042,211A  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: JP 2001-088912  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/254018  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: JP 2001-042288  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/278,640  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/314,385  
 ; PRIOR FILING DATE: 2001-08-24  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 178  
 ; LENGTH: 129  
 ; Query Match 93.9%; Score 571; DB 15; Length 129;  
 ; Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 ; Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-10-331-496A-37  
 ; Sequence 37, Application US/10331496A  
 ; Publication No. US20030228305A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANTZ, GRETCHEN  
 ; APPLICANT: HILLIAN, KENNETH J.  
 ; APPLICANT: PHILLIPS, HEIDI S.  
 ; APPLICANT: POLAKIS, PAUL  
 ; APPLICANT: SMITH, VICTORIA  
 ; APPLICANT: SPENCER, SUSAN D.  
 ; APPLICANT: WILLIAMS, P. MICKEY  
 ; APPLICANT: WU, THOMAS D.  
 ; APPLICANT: ZHANG, ZEMIN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 ; FILE REFERENCE: P5014R1-PCT  
 ; CURRENT APPLICATION NUMBER: US/10/331,496A  
 ; CURRENT FILING DATE: 2002-12-30  
 ; PRIOR APPLICATION NUMBER: US 60/345,444  
 ; PRIOR FILING DATE: 2002-01-02  
 ; PRIOR APPLICATION NUMBER: US 60/351,885  
 ; PRIOR FILING DATE: 2002-01-25  
 ; PRIOR APPLICATION NUMBER: US 60/360,066  
 ; PRIOR FILING DATE: 2002-02-25  
 ; PRIOR APPLICATION NUMBER: US 60/362,004  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/366,869  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/366,284  
 ; PRIOR FILING DATE: 2002-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/368,679  
 ; PRIOR FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/404,809  
 ; PRIOR FILING DATE: 2002-08-19  
 ; PRIOR APPLICATION NUMBER: US 60/405,645  
 ; PRIOR FILING DATE: 2002-08-21  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SEQ ID NO 37  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-10-331-496A-37  
 ; Sequence 37, Application US/10331496A  
 ; Publication No. US20030228305A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATSUDA, Akio et al.  
 ; TITLE OF INVENTION: NFkB Activating Gene  
 ; FILE REFERENCE: 1254-0192P  
 ; CURRENT APPLICATION NUMBER: US/10/042,211A  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: JP 2001-088912  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/254018  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: JP 2001-042288  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/278,640  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/314,385  
 ; PRIOR FILING DATE: 2001-08-24

Qy 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRRESSPPP 113  
 Db 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRREKFTTP 113

## RESULT 8

US-10-295-027-444

; Sequence 444, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynne, Richard

; APPLICANT: Hevezzi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; Modulators of Cancer

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIORITY APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIORITY APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIORITY APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIORITY APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIORITY APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIORITY APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIORITY APPLICATION NUMBER: US 60/332,464

; PRIOR FILING DATE: 2001-11-21

; PRIORITY APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIORITY APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIORITY APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIORITY APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2001-12-14

; PRIORITY APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIORITY APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10

; PRIORITY APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08

; PRIORITY APPLICATION NUMBER: US 60/356,714

; PRIOR FILING DATE: 2002-02-13

; PRIORITY APPLICATION NUMBER: US 60/356,714

; PRIORITY APPLICATION NUMBER: US 1386

; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsberg, Wendy M.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Glynne, Richard  
 ; APPLICANT: Hevezzi, Peter A.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
 ; Modulators of Cancer  
 ; FILE REFERENCE: 018501-012500US  
 ; CURRENT APPLICATION NUMBER: US/10/295,027  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIORITY APPLICATION NUMBER: US 09/663,733  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIORITY APPLICATION NUMBER: US 60/350,666  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIORITY APPLICATION NUMBER: US 60/335,394  
 ; PRIOR FILING DATE: 2001-11-21  
 ; PRIORITY APPLICATION NUMBER: US 60/334,393  
 ; PRIOR FILING DATE: 2001-11-29  
 ; PRIORITY APPLICATION NUMBER: US 60/340,376  
 ; PRIOR FILING DATE: 2001-12-14  
 ; PRIORITY APPLICATION NUMBER: US 60/347,211  
 ; PRIOR FILING DATE: 2002-01-10  
 ; PRIORITY APPLICATION NUMBER: US 60/355,250  
 ; PRIOR FILING DATE: 2002-02-08  
 ; PRIORITY APPLICATION NUMBER: US 60/356,714  
 ; PRIOR FILING DATE: 2002-02-13  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1386  
 ; SEQ ID NO 444  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-295-027-444

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Qy 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRRESSPPP 113  
 Db 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRREKFTTP 113

Query Match 93.9%; Score 571; DB 15; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 9  
 US-10-295-027-1305

1 Sequence 5, Application US/09742454A  
 ; Patent No. US20020041876A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: TWEAK Receptor  
 ; FILE REFERENCE: 296B-B  
 ; CURRENT APPLICATION NUMBER: US/09/742,454A  
 ; CURRENT FILING DATE: 2000-12-19  
 ; PRIORITY APPLICATION NUMBER: US/09/742,454A-5

1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSFLVWRRCRRESSPPP 113  
 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSFLVWRRCRREKFTTP 113

Qy 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRREKFTTP 113  
 Db 61 SDFCLGCAAAPPAPFLWPILGALSLTFVLGLLSGFLVWRRCRREKFTTP 113

Query Match 93.9%; Score 571; DB 15; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 6.3e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 8  
 US-10-295-027-1305

1 Sequence 1305, Application US/10295027  
 ; Publication No. US20030232350A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Afar, Daniel

; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Mus sp.  
 US-09-742-454A-5

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 Best Local Similarity 75.2%; Pred. No. 3.4e-36;  
 Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
 ; OTHER INFORMATION: receptor fusion protein construct  
 US-09-742-454A-7

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Qy 61 SDFCLGCAAAPPAPFRLLWPILGGALSITFVLGLSGFLVWRRCRRERSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLLWPILGGALSIVLAVSSFLVWRRCRRREKFPTTP 113

RESULT 11  
 ; Sequence 5, Application US/09883777  
 ; Patent No. US20020110853A1

GENERAL INFORMATION:  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: TWEAK RECEPTOR  
 ; FILE REFERENCE: 2968-C

CURRENT APPLICATION NUMBER: US/09/883,777  
 CURRENT FILING DATE: 2001-06-18  
 PRIOR APPLICATION NUMBER: US 60/172,878  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: US 60/203,347  
 PRIOR FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: PCT/US00/34755  
 PRIOR FILING DATE: 2000-12-19  
 PRIOR APPLICATION NUMBER: US 09/742,454  
 PRIOR FILING DATE: 2000-12-19  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 129  
 TYPE: PRT  
 ORGANISM: Mus sp.  
 US-09-883-777-5

Query Match 74.0%; Score 450; DB 9; Length 129;  
 Best Local Similarity 75.2%; Pred. No. 3.4e-36;  
 Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

; FEATURE:  
 ; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
 US-09-883-777-7

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 Db 1 MAPGWPRSLPQILVLMRAAAGEQAPGTTSPCSSGGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAPPAPFRLLWPILGGALSITFVLGLSGFLVWRRCRRERSPPP 113  
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RESULT 12  
 US-09-742-454A-7

; Sequence 7, Application US/09742454A  
 ; Patent No. US20020041876A1

GENERAL INFORMATION:  
 ; APPLICANT: WILEY, Steven R.  
 ; TITLE OF INVENTION: TWEAK Receptor  
 ; FILE REFERENCE: 2968-B

CURRENT APPLICATION NUMBER: US/09/742,454A  
 CURRENT FILING DATE: 2000-12-19  
 PRIOR APPLICATION NUMBER: 1999-12-20  
 PRIOR FILING DATE: 1999-12-19  
 PRIOR APPLICATION NUMBER: 60/203,347  
 PRIOR FILING DATE: 2000-05-10  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7  
 ; LENGTH: 309  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence

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 Best Local Similarity 74.1%; Pred. No. 3.7e-34;  
 Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

; FEATURE:  
 ; OTHER INFORMATION: receptor fusion protein construct  
 US-09-742-454A-7

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 Db 1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAPPAPFRLLWPILGGALSITFVLGLSGFLVWRRCRRERSPPP 112  
 Db 61 SDFCLGCAAAPPAPFRLLWPILGGALSITFVLGLSGFLVWRRCRRERSPPP 112

RESULT 14  
 US-09-883-777-9

; Sequence 9, Application US/09883777  
 ; Patent No. US20020110853A1

GENERAL INFORMATION:  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: TWEAK RECEPTOR  
 ; FILE REFERENCE: 2968-C

CURRENT APPLICATION NUMBER: US/09/883,777  
 CURRENT FILING DATE: 2001-06-18

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; PRIORITY APPLICATION NUMBER: US 60/172, 878
; PRIORITY FILING DATE: 1999-12-20
; PRIORITY APPLICATION NUMBER: US 60/203, 347
; PRIORITY FILING DATE: 2000-05-10
; PRIORITY APPLICATION NUMBER: PCT/US00/34755
; PRIORITY FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/742, 454
; PRIORITY FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

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Best Local Similarity 88.0%; Pred. No. 5.6e-29;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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Db          1 MARGSLRRRLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

QY          61 SDFCLGCAA-----PPAP 74
Db          61 SDFCLGCAAARSCKTHTCPCP 83

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## RESULT 15

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US-10-251-947-4
; Sequence 4, Application US/10251947
; Publication No: US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: HSU, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-4

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Matches 34; Conservative 9; Mismatches 39; Indels 25; Gaps 5;
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QY          81 -----ILGGA---LSLTFLVGL-LSGFLVMRRCRER 108
Db          63 SVGTGSGEVSLPLPGLLFGAPALLGLVVLVGLVSWRR-RQQR 108

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GenCore version 5.1.6  
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Run on: March 1, 2004, 16:42:58 ; Search time 181 Seconds  
(without alignments)  
614.752 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608  
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Total number of hits satisfying chosen parameters: 6019581

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Post-processing: Minimum Match 0%

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Sequence 631, App  
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Sequence 1305, App  
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Sequence 9, App1  
Sequence 4883, App  
Sequence 4884, App  
Sequence 1095, App  
Sequence 1582, App  
Sequence 507, App  
Sequence 136, App  
Sequence 139, App  
Sequence 3456, App  
Sequence 1096, App  
Sequence 1583, App  
Sequence 508, App  
Sequence 277, App

#### ALIGNMENTS

#### RESULT 1

PCT-US98-10868-60  
; Sequence 60, Application PC/TUSS9810868

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc., et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/10868  
FILING DATE: May 27, 1998  
CLASSIFICATION:

#### SUMMARIES

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4	99.8	114	26 US-10-062-831-59	
5	93.9	129	1 PCT-US02-08277-745	
6	93.9	129	1 PCT-US02-08278-1079	
7	93.9	129	1 PCT-US02-08279-349	
8	93.9	129	1 PCT-US02-41798A-37	
9	93.9	129	17 US-09-307-140-627	
10	93.9	129	17 US-09-316-633-265	
11	93.9	129	18 US-09-445-258-16	
12	93.9	129	18 US-09-445-258A-16	
13	93.9	129	18 US-09-465-587-220	
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28	93.9	129	33 US-60-109-869-2	
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35	93.6	55.3	94 30 US-10-405-027-4884	
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#### SUMMARIES

Result	Score	Match Length	DB ID	Description
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2	99.8	114	15 US-09-189-144-59	
3	99.8	114	26 US-10-062-599-59	
4	99.8	114	26 US-10-062-831-59	
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20	93.9	129	26 US-10-042-211A-178	
21	93.9	129	27 US-10-126-052A-631	
22	93.9	129	28 US-10-295-027-444	
23	93.9	129	29 US-10-295-027-1305	
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PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PZ006PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; PCT-US98-10868-60

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Query Match 99.8%; Score 607; DB 1; Length 114;  
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Db	1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60
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RESULT 3  
US-10-062-599-59  
; Sequence 59, Application US/10062599  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062,599  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
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; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation

US-10-062-599-59  
Query Match 99.8%; Score 607; DB 26; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.9e-51;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60
Db	1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60
Qy	61 SDFCLGCAAAPPAPFRLLWPI LGGALS LT FVL GLLSGFLV WRR CRERSS PPP 113
Db	61 SDFCLGCAAAPPAPFRLLWPI LGGALS LT FVL GLLSGFLV WRR CRERSS PPP 113

RESULT 4  
US-10-062-831-59  
; Sequence 59, Application US/10062831  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; OTHER INFORMATION: Xaa equals stop translation  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation

Query Match 99.8%; Score 607; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.9e-51;

FILE REFERENCE: PZ006P1  
 CURRENT APPLICATION NUMBER: US/10/062, 831  
 CURRENT FILING DATE: 2002-02-05  
 PRIOR APPLICATION NUMBER: 09/690, 454  
 PRIOR FILING DATE: 1998-11-10  
 PRIOR APPLICATION NUMBER: PCT/US98/10868  
 PRIOR FILING DATE: May 28, 1998  
 PRIOR APPLICATION NUMBER: 60/044, 039  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/048, 093  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/04B, 190  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/050, 935  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/048, 101  
 PRIOR FILING DATE: May 30, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 250  
 PRIOR FILING DATE: August 29, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 296  
 PRIOR FILING DATE: August 29, 1997  
 PRIOR APPLICATION NUMBER: 60/056, 293  
 PRIOR FILING DATE: August 29, 1997  
 NUMBER OF SEQ ID NOS: 229  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 59  
 LENGTH: 114  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (114)  
 OTHER INFORMATION: Xaa equals stop translation  
 US-10-062-831-59

Query Match 99.8%; Score 607; DB 26; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113

RESULT 5  
 PCT-US02-08277-745  
 ; Sequence 745, Application PC/TUS0208277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Human Secreted Proteins  
 ; FILE REFERENCE: PS907PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US02/08277  
 ; CURRENT FILING DATE: 2002-03-19  
 ; PRIOR APPLICATION NUMBER: US 60/331, 287  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/306, 171  
 ; PRIOR FILING DATE: 2001-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/277, 340  
 ; PRIOR FILING DATE: 2001-03-21  
 ; NUMBER OF SEQ ID NOS: 642  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 745  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; PCT-US02-08277-745

Query Match 93.9%; Score 571; DB 1; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113

RESULT 6  
 PCT-US02-08278-1079  
 ; Sequence 1079, Application PC/TUS0208278  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Human Secreted Proteins  
 ; FILE REFERENCE: PS902PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US02/08278  
 ; CURRENT FILING DATE: 2002-03-19  
 ; PRIOR APPLICATION NUMBER: US 60/331, 287  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/306, 171  
 ; PRIOR FILING DATE: 2001-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/277, 340  
 ; PRIOR FILING DATE: 2001-03-21  
 ; NUMBER OF SEQ ID NOS: 1988  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1079  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; PCT-US02-08278-1079

Query Match 93.9%; Score 571; DB 1; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60  
 Db 1 MARGSLRRRLVGLWLLALLRSVAQEAPGTAPCSRSQSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLWRRCRRERSSPPP 113

RESULT 7  
 PCT-US02-08279-349  
 ; Sequence 349, Application PC/TUS0208279  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Human Secreted Proteins  
 ; FILE REFERENCE: PS903PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US02/08279  
 ; CURRENT FILING DATE: 2002-03-19  
 ; PRIOR APPLICATION NUMBER: US 60/331, 287  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/306, 171  
 ; PRIOR FILING DATE: 2001-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/277, 340  
 ; PRIOR FILING DATE: 2001-03-21  
 ; NUMBER OF SEQ ID NOS: 642  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 349  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; PCT-US02-08279-349

Query Match 93.9%; Score 571; DB 1; Length 129;

Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60  
 .Db 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113

RESULT 8  
 PCT-US02-41798A-37  
 ; Sequence 37, Application PC/TUS0241798A

; GENERAL INFORMATION:

; APPLICANT: FRANTZ, GRETCHEN  
 ; APPLICANT: HILLAN, KENNETH J.  
 ; APPLICANT: PHILLIPS, HEIDI S.  
 ; APPLICANT: POLAKIS, PAUL  
 ; APPLICANT: SMITH, VICTORIA  
 ; APPLICANT: SPENCER, SUSAN D.  
 ; APPLICANT: WILLIAMS, P. MICKEY  
 ; APPLICANT: WU, THOMAS D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TREATMENT OF TUMOR

; FILE REFERENCE: P5014R1-PCT

; CURRENT APPLICATION NUMBER: PCT/US02/41798A

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: US 60/345,444

; PRIOR FILING DATE: 2002-01-02

; PRIOR APPLICATION NUMBER: US 60/351,885

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: US 60/360,066

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: US 60/362,004

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/366,869

; PRIOR FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: US 60/366,284

; PRIOR FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: US 60/368,679

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 60/404,809

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: US 60/405,645

; PRIOR FILING DATE: 2002-08-21

; NUMBER OF SEQ ID NOS: 95

; SEQ ID NO 37

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Homo sapien

PCT-US02-41798A-37

Query Match 93.9%; Score 571; DB 1; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60  
 .Db 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113

RESULT 9

US-09-307-140-627

; Sequence 627, Application US/09307140

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60  
 .Db 1 MARGSLRRLRLJLVLGLWLALLRSVAGEQAPGTAPCSRGGSSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTTFVLGLLSGFLVWRRCRREKFTTP 113

RESULT 11

US-09-445-258-16

Sequence 1.6, Application US/09445258  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Seishi  
; APPLICANT: Sekine, Shingo  
; APPLICANT: Kimura, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE  
; DOMAINS AND DNAs ENCODING THESE PROTEINS  
; FILE REFERENCE: GIN-6706CPUS  
; CURRENT APPLICATION NUMBER: US/09/445, 258  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US98/02445  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: JP 9-144948  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-445-258-16

Query Match 93.9%; Score 571; DB 18; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Db 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Qy 61 SDFCLGCAAAPPAPFLWPILGGALSLT  
Db 61 SDFCLGCAAAPPAPFLWPILGGALSLT

Query Match 93.9%; Score 571; DB 18; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Db 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Qy 61 SDFCLGCAAAPPAPFLWPILGGALSLT  
Db 61 SDFCLGCAAAPPAPFLWPILGGALSLT

RESULT 1.2  
US-09-445-258A-16  
; Sequence 1.6, Application US/09445258A  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Seishi  
; APPLICANT: Sekine, Shingo  
; APPLICANT: Kimura, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE  
; DOMAINS AND DNAs ENCODING THESE PROTEINS  
; FILE REFERENCE: GIN-6706CPUS  
; CURRENT APPLICATION NUMBER: US/09/445, 258A  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US98/02445  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-445-258A-16

Query Match 93.9%; Score 571; DB 18; Length 129;  
Best Local Similarity 94.7%; Pred. No. 3.3e-47;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Db 1 MARGSLRRLRLVGLWLALLRSVAQEAPGTA  
Qy 61 SDFCLGCAAAPPAPFLWPILGGALSLT  
Db 61 SDFCLGCAAAPPAPFLWPILGGALSLT

RESULT 14  
US-09-700-590A-64  
; Sequence 64, Application US/09700590A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: LAL, Preeti  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: YUE, Henry  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: GORGONE, Gina A.  
; APPLICANT: KASER, Matthew R.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AU-YOUNG, Janice  
; TITLE OF INVENTION: HUMAN TRANSMEMBRANE PROTEINS  
; FILE REFERENCE: PF-0526 USN  
; CURRENT APPLICATION NUMBER: US/09/700, 590A  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/087, 260  
; PRIOR FILING DATE: 05-29-1998  
; PRIOR APPLICATION NUMBER: 60/091, 674  
; PRIOR FILING DATE: 07-02-1998  
; PRIOR APPLICATION NUMBER: 60/102, 954  
; PRIOR FILING DATE: 10-02-1998  
; PRIOR APPLICATION NUMBER: 60/109, 869  
; PRIOR FILING DATE: 11-24-1998  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: PERL Program  
; SEQ ID NO 64  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

RESULT 1.3

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2454048
US-09-700-590A-64

Query Match      93.9%;  Score 571;  DB 21;  Length 129;
Best Local Similarity 94.7%;  Pred. No. 3.3e-47;
Matches 107;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy          1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60
Db          1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy          61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSSPPP 113
Db          61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRRCRREREKFTTP 113

RESULT 15
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      93.9%;  Score 571;  DB 21;  Length 129;
Best Local Similarity 94.7%;  Pred. No. 3.3e-47;
Matches 107;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy          1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60
Db          1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy          61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSSPPP 113
Db          61 SDFCLGCAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRRCRREREKFTTP 113

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Search completed: March 1, 2004, 16:48:23  
Job time : 182 secs

Copyright (c) 1993 - 2004 CompuGen Ltd.  
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 on: March 1, 2004, 16:43:08 ; Search time 10 Seconds  
 (without alignments)  
 102.796 Million cell updates/sec  
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 perfect score: 608  
 sequence: 1 MARGSLRLLRLLVGLWIA..... LSGFILVWRRCRRERSSSPPPX 114  
 scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 searched: 99762 seqs, 9017151 residues

Total number of hits satisfying chosen parameters: 99762

maximum DB seq length: 0  
maximum DB seq length: 2000000000

RESULT 1

st-processing: Minimum Match 0% ; Sequence 33810, Application US/10767701  
Maximum Match 100% ; GENERAL INFORMATION:  
Histogram First 45 summaries

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2: /cgn2\_6/ptodata/1/paa/US06 NEW COMB.pep:  
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4: /cgn2\_6/ptodata/1/paa/US08 NEW COMB.pep:  
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7: /cgn2\_6/ptodata/1/paa/US60 NEW COMB.pep:  
  
tabase : Pending Patents AA\_New:  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Improvement Of Plants and Uses Thereof For Plant Improvement  
FILE REFERENCE: 38-21(53535) B  
CURRENT APPLICATION NUMBER: US/10/767,701  
CURRENT FILING DATE: 2004-01-29  
NUMBER OF SEQ ID NOS: 63128

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ESTIMATES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	13.8	152	US-10-767-701-33810	Sequence 33810, A
2	71	11.7	123	US-10-773-236-290	Sequence 290, APP
3	67.5	11.1	368	US-10-667-762-10	Sequence 10, Appl
4	66.5	10.9	229	US-10-767-701-46659	Sequence 46659, A
5	66	10.9	1238	US-10-762-603-4	Sequence 4, Appl
6	65.5	10.8	271	US-10-417-375A-11	Sequence 11, Appl
7	65	10.7	189	US-10-767-701-43640	Sequence 43640, A
8	64.5	10.6	1417	US-10-767-471-1010	Sequence 1010, AP
9	64.5	10.6	1421	US-10-767-471-1009	Sequence 1009, AP
10	64.5	10.6	1557	US-10-767-471-1011	Sequence 1011, AP
11	64.5	10.6	1557	US-10-767-471-1014	Sequence 1014, AP
12	64.5	10.6	1587	US-10-767-471-1013	Sequence 1013, AP
13	64.5	10.6	1587	US-10-767-471-1015	Sequence 1015, AP
14	64.5	10.6	1664	US-10-767-471-1012	Sequence 1012, AP
15	64	10.5	115	US-10-333-177-2	Sequence 2, Appl
16	63.5	10.4	126	US-10-767-701-60623	Sequence 60623, A
17	63.5	10.4	138	US-10-767-701-58471	Sequence 58471, A
18	63.5	10.4	150	US-10-767-701-54494	Sequence 54494, A
19	63.5	10.4	161	US-10-767-701-41647	Sequence 41647, A
20	63.5	10.4	193	US-10-767-701-33811	Sequence 33811, A
21	63.5	10.4	390	US-10-767-701-38237	Sequence 38237, A
22	63.5	10.4	476	PCT-US04-03417-8	Sequence 8, Appl
23	63.5	10.4	476	US-10-772-636-8	Sequence 8, Appl
24	62.5	10.3	283	US-10-451-467A-76	Sequence 76, Appl
25	62.5	10.3	355	US-10-767-701-37723	Sequence 37723, A
26	62.5	10.3	954	US-10-767-701-91022	Sequence 91022, A

RESULT 2  
US-10-773-236-290  
; Sequence 290, Application US/10773236  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al.  
; TITLE OF INVENTION: 89 Human Secrete  
; FILE REFERENCE: PS751P1  
; CURRENT APPLICATION NUMBER: US/10/77  
; CURRENT FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/311,085  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,209  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: PCT/US02/2  
; PRIOR FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/330,629  
 PRIOR FILING DATE: 2001-10-26  
 PRIOR APPLICATION NUMBER: PCT/US02/33985  
 PRIOR FILING DATE: 2002-10-24  
 PRIOR APPLICATION NUMBER: 60/331,046  
 PRIOR FILING DATE: 2002-11-07  
 PRIOR APPLICATION NUMBER: PCT/US02/35606  
 PRIOR FILING DATE: 2002-11-06  
 PRIOR APPLICATION NUMBER: 60/358,554  
 PRIOR FILING DATE: 2002-02-22  
 PRIOR APPLICATION NUMBER: PCT/US03/04819  
 PRIOR FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/358,714  
 PRIOR FILING DATE: 2002-02-25  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 396  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 290  
 LENGTH: 123  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (55)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (101)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 US-10-773-236-290

Query Match 11.7%; Score 71; DB 6; Length 123;  
 Best Local Similarity 32.0%; Pred. No. 1-6;  
 Matches 24; Conservative 5; Mismatches 26; Indels 20; Gaps 5;

Qy	31	PGTAPCSRGSWSAD--LDKCMDC--ASCRARPHSDFCLG-----CAAAP	71
:	:	:	:
Db	40	PGWSWCSPSLIGSWCXTEGLLRCLQAAVATCPRCPTSDLLGRAWSSWORTLLCCPGP	99

Query Match 11.1%; Score 67.5; DB 6; Length 368;  
 Best Local Similarity 34.4%; Pred. No. 9-6;  
 Matches 21; Conservative 2; Mismatches 23; Indels 15; Gaps 2;

Qy	65	LGCAAPP-----APFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSP	111
:	:	:	:
Db	149	LGPPPPAPPAPARCSVLAGGLGPFRPLWALLAFAFPALLLGAYGGIFV--VARRAALRP	206

Query Match 10.9%; Score 66.5; DB 6; Length 229;  
 Best Local Similarity 28.7%; Pred. No. 7-7;  
 Matches 25; Conservative 8; Mismatches 29; Indels 25; Gaps 3;

Qy	39	GSSWSADLD-KMDCASCR-----ARPHSDFCLGCAAAPPAPFILLWPIL-----	82
:	:	:	:
Db	104	GAAWSTLKEFKVNESYSCRYMLGSNKADIHSKLFNCTAEEPSTTELLKRILLFSEMYV	163

RESULT 3  
 US-10-667-762-10  
 Sequence 10, Application US/10667762  
 GENERAL INFORMATION:  
 APPLICANT: Erding Hu  
 APPLICANT: Yuan Zhu  
 APPLICANT: Ganesh M. Sathe  
 APPLICANT: Joyce Yue Mao  
 APPLICANT: Wendy S. Halsey  
 APPLICANT: Jon Chambers  
 APPLICANT: Alison Isobel Muir  
 APPLICANT: Philip Graham Szekeres  
 APPLICANT: Usman Shabon  
 APPLICANT: Derk J. Bergsma  
 APPLICANT: Nabil A. Elshourbagy  
 APPLICANT: David Michalovich  
 APPLICANT: Pamela A. Lane  
 APPLICANT: Menelas N. Pangalos  
 APPLICANT: Melanie Robbins  
 APPLICANT: David Malcolm Duckworth  
 APPLICANT: Jeffrey Hill  
 APPLICANT: Ping Tsui  
 APPLICANT: Pankaj Agarwal  
 APPLICANT: Randall Forrest Smith  
 APPLICANT: Lisa Vawter  
 APPLICANT: Catherine E. Ellis  
 APPLICANT: Manhanandeeeshwar Gattu  
 APPLICANT: John W. Quillen, Jr.  
 APPLICANT: Erin M. Toland

RESULT 4  
 US-10-767-701-46659  
 Sequence 46659, Application US/10767701  
 GENERAL INFORMATION:  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: Plants and Uses Thereof For Plant Improvement  
 CURRENT APPLICATION NUMBER: US/10/767,701  
 CURRENT FILING DATE: 2004-01-29  
 NUMBER OF SEQ ID NOS: 63128  
 SEQ ID NO: 46659  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Sorghum bicolor  
 FEATURE:  
 OTHER INFORMATION: Clone ID: SORBI-2BMAY03-C104\_76.pep  
 US-10-767-701-46659

Qy 83 -----GGALSLTFTVGLLSSGFLV 100  
 Db 164 SEDSSEERMLGYVAAGWVIGMILSSMFI 190

RESULT 5  
 US-10-762-603-4  
 ; Sequence 4, Application US/10762603  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nickoloff, Brian  
 ; APPLICANT: Milele, Lucio  
 ; TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENT OF MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATHWAY  
 ; FILE REFERENCE: 225907  
 ; CURRENT APPLICATION NUMBER: US/10/762,603  
 ; CURRENT FILING DATE: 2004-01-22  
 ; PRIOR APPLICATION NUMBER: US 60/229,614  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: US 09/944,849  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 4  
 ; LENGTH: 1238  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-762-603-4

Query Match 10.9%; Score 66; DB 6; Length 1238;  
 Best Local Similarity 24.6%; Pred. No. 41;  
 Matches 34; Conservative 5; Mismatches 35; Indels 64; Gaps 5;

Qy 3 RGSIRRLLRLVLGLW-----LALLRSVAGEQAPG----- 32  
 Db 6 RGRIPRRL-LLLLALWVQAARPMGYFELQLSAQRNNGEILLSGACCDGDGRTTRAGGCGH 64

Qy 33 -----TAPCSRQ-----SSWSADLDKCMDCASCRAPHSD 62  
 Db 65 DECDDTYVRVCLKEYQAKYTPGCSYGHGATPPVLAGNSFYLPPAGAAAGDRARARAGGD 124

Qy 63 FCLGCAAAPPAPERLWP 80  
 Db 125 QDPGLVV---IPFQFAWP 139

RESULT 6  
 US-10-417-375A-11  
 ; Sequence 11, Application US/10417375A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: David W. Morris  
 ; APPLICANT: Marc Malandro  
 ; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
 ; FILE REFERENCE: 529452001600  
 ; CURRENT APPLICATION NUMBER: US/10/417,375A  
 ; CURRENT FILING DATE: 2003-04-15  
 ; NUMBER OF SEQ ID NOS: 176  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 271  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-417-375A-11

Query Match 10.8%; Score 65.5; DB 6; Length 271;  
 Best Local Similarity 26.8%; Pred. No. 11;  
 Matches 22; Conservative 11; Mismatches 10; Indels 39; Gaps 5;

Qy 13 LVGLWLALLRSVAGE-----QAPG-----TAPCSRGSWSAD 45  
 Db 40 ILLGLWLAVLPTLAGDKLILSVCMNSKRHKQEPGPEDELYQECRPWEDDNACCTRSTSWEAH 98

Qy 46 LDK-----CMDCA----SCR 56  
 Db 99 LEEPLFNFSMMHCGLLTPACR 120

RESULT 7  
 US-10-767-701-43640  
 ; Sequence 43640, Application US/10767701  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovacic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement  
 ; FILE REFERENCE: 38-21(53535)B  
 ; CURRENT APPLICATION NUMBER: US/10/767,701  
 ; CURRENT FILING DATE: 2004-01-29  
 ; NUMBER OF SEQ ID NOS: 63128  
 ; SEQ ID NO 43640  
 ; LENGTH: 189  
 ; TYPE: PRT  
 ; ORGANISM: Sorghum bicolor  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C81491\_1.pep  
 US-10-767-701-43640

Query Match 10.7%; Score 65; DB 6; Length 189;  
 Best Local Similarity 29.4%; Pred. No. 9;  
 Matches 30; Conservative 5; Mismatches 35; Indels 32; Gaps 5;

Qy 30 APGTAFCSRG----SSWSADLDKCMDCA-----SCRARPHSDFCLGCAAAPPAPF-- 75  
 Db 24 AASTAPSFGKGGRDGAASAPACCGCARRPVHLPPAALARLPPEG--ACRAAAPGAPAVR 81

Qy 76 -----RLLWPILLGGALSLSTFVLLGSGFLVWRR 103  
 Db 82 AAPGAVRVSACALPRDLPLLAGGARPA--ALPSLCKLRVWRR 121

RESULT 8  
 US-10-767-471-1010  
 ; Sequence 1010, Application US/10767471  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001505  
 ; CURRENT APPLICATION NUMBER: US/10/767,471  
 ; CURRENT FILING DATE: 2004-01-30  
 ; NUMBER OF SEQ ID NOS: 50231  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1010  
 ; LENGTH: 1417  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (1..1417)  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 US-10-767-471-1010

Query Match 10.6%; Score 64.5; DB 6; Length 1417;  
 Best Local Similarity 29.7%; Pred. No. 65;  
 Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSWSADLDKCMDCASCRAPHSDFCLG-----AAAPPAPFRLLWPILLGGALSLT 89  
 Db 1088 CLYGEAWG----MDCALCPAQDSDDFEALCNVLRPPAYSPPR-----GGFGLP 1132

Qy 90 FVLG 93  
 Db 1133 YEYG 1136

RESULT 9  
US-10-767-471-1009  
Sequence 1009, Application US/10767471  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001505  
CURRENT APPLICATION NUMBER: US/10/767,471  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 50231  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1009  
LENGTH: 1421  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-767-471-1014

Query Match 10.6%; Score 64.5; DB 6; Length 1421;  
Best Local Similarity 29.7%; Pred. No. 65;  
Matches 19; Conservative 4; MisMatches 20; Indels 21; Gaps 3;

RESULT 10  
US-10-767-471-1011  
Sequence 1011, Application US/10767471  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001505  
CURRENT APPLICATION NUMBER: US/10/767,471  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 50231  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1011  
LENGTH: 1557  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-767-471-1011

Query Match 10.6%; Score 64.5; DB 6; Length 1557;  
Best Local Similarity 29.7%; Pred. No. 70;  
Matches 19; Conservative 4; MisMatches 20; Indels 21; Gaps 3;

RESULT 11  
US-10-767-471-1014  
Sequence 1014, Application US/10767471  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001505  
CURRENT APPLICATION NUMBER: US/10/767,471  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 50231  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1014

Query Match 10.6%; Score 64.5; DB 6; Length 1557;  
Best Local Similarity 29.7%; Pred. No. 72;  
Matches 19; Conservative 4; MisMatches 20; Indels 21; Gaps 3;

RESULT 12  
US-10-767-471-1013  
Sequence 1013, Application US/10767471  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001505  
CURRENT APPLICATION NUMBER: US/10/767,471  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 50231  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1013

Query Match 10.6%; Score 64.5; DB 6; Length 1587;  
Best Local Similarity 29.7%; Pred. No. 72;  
Matches 19; Conservative 4; MisMatches 20; Indels 21; Gaps 3;

RESULT 13  
US-10-767-471-1015  
Sequence 1015, Application US/10767471  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001505  
CURRENT APPLICATION NUMBER: US/10/767,471  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 50231  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1015

Query Match 10.6%; Score 64.5; DB 6; Length 1587;  
Best Local Similarity 29.7%; Pred. No. 72;  
Matches 19; Conservative 4; MisMatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSWSADLDKCMDCASCARPHSDFCLGC-----AAAPPAPFRLLWPILGALS LT 89  
 Db 1340 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRRPAYSPPRP-----GGFGLP 1384

Qy 90 FVLG 93  
 Db 1385 YEYG 1388

RESULT 14  
 US-10-767-471-1012  
 ; Sequence 1012, Application US/10767471  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001505  
 ; CURRENT APPLICATION NUMBER: US/10/767,471  
 ; CURRENT FILING DATE: 2004-01-30  
 ; NUMBER OF SEQ ID NOS: 50231  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 1012  
 ; LENGTH: 1664  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (1) : (1664)  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 US-10-767-471-1012

Query Match 10.6%; Score 64.5; DB 6; Length 1664;  
 Best Local Similarity 29.7%; Pred. No. 75;  
 Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSWSADLDKCMDCASCARPHSDFCLGC-----AAAPPAPFRLLWPILGALS LT 89  
 Db 1335 CLYGEAWG-----MDCALCPAQDSDDFEALCNVLRRPAYSPPRP-----GGFGLP 1379

Qy 90 FVLG 93  
 Db 1380 YEYG 1383

RESULT 15  
 US-10-333-177-2  
 ; Sequence 2, Application US/10333177  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Riissoan, Marie-Clotilde  
 ; APPLICANT: Bridon, Jean-Michel  
 ; APPLICANT: Duhen, Thomas  
 ; APPLICANT: Briere, Francine  
 ; APPLICANT: Bates, Elizabeth  
 ; TITLE OF INVENTION: Type 2 Dendritic Cell Precursor Derived Coding Nucleic Acids and Compositions and Methods  
 ; FILE REFERENCE: SF01190  
 ; CURRENT APPLICATION NUMBER: US/10/333,177  
 ; CURRENT FILING DATE: 2003-01-16  
 ; PRIOR APPLICATION NUMBER: EP 00306087.8  
 ; PRIOR FILING DATE: 2000-07-18  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 115  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-333-177-2

Query Match 10.5%; Score 64; DB 6; Length 115;  
 Best Local Similarity 30.8%; Pred. No. 7;  
 Matches 16; Conservative 3; Mismatches 23; Indels 10; Gaps 2;



Page 2

A;Accession: B70939  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-436 <COL>  
A;Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PID:CAA17338.1; PID:e125244;  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0246

```

;189-205/Domain: transmembrane #status predicted <TM3>
;212-228/Domain: transmembrane #status predicted <TM4>
Query Match 12.6%; Score 76.5; DB 2; Length 245;
Best Local Similarity 30.8%; Pred. No. 4.3;
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;
Query Match 12.4%; Score 75.5; DB 2; Length 436;
Best Local Similarity 23.0%; Pred. No. 8.4;
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;
QY 1 MARGSLRRLRLLVGLWLAIIRSSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR 56
Db 142 MPSGTARARILLTEVGVAALTAVVAATLSFVFDQHPLSRNITHLWTAAVAMAISAAICR 201
QY 57 ARPHSDDFCLGCAAAPPAPERFLWW----PIUGG---- 84
Db 202 ALPHR--IVPRVHAAPGLHKLVYVGWTAIRTNGWYRRYLLVQVLFGSVVILGSSFHISRVA 259
QY 85 -----ALSLTFFVGLLSSGFLVWRRRCR 105
Db 260 AVPGDQPDEWVAVVLFVCGLLGGIALWNVR 291

```

RESULT 3  
D0753  
Flagellar biosynthetic protein FlIP [imported] - *Salmonella enterica* serovar Typhi  
Species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
Note: this species has also been called *Salmonella typhi*  
Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
Accession: AD0753  
; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
ature 413, 848-852, 2001  
; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi  
; Reference number: AB0502; MUID:21534947; PMID:11677608

;Accession: AD0753  
;Status: preliminary  
;Molecule type: DNA  
;Residues: 1-245 <PAR>  
;Cross-references: GB:AL513382; PIDN:CAD05727.1; P  
;Genetics:  
;Gene: STY2187

Query	Match	12.6%	Score	76.5	DB	2	Length	245	
Best Local	Similarity	30.8%	Pred. No.	4.3					
Matches	33	Conservative	9	Mismatches	38	Indels	27	Gaps	6
Y	6	LRRLLRLVGLWLALLRSVAGEQAPG--TAP-CSRGSWSADLDDKCMDCACCRARP---	59						
b	1	MRRLLFLSLAGLW-LFESPAAAQLPGLISQPLAGGQSWSSLSVQTLVFTISLTFLPAIL	58						
Y	60	--HSDF-----CLGCAAAPPAPPERRLLWPILGGALS LT FVT	92						
b	59	I MMTSETB IIIIVFGI L R N A U G T P S A P P N O V -----LLGIA LF L F E E I	100						

RESULT 4  
70939  
Hypothetical protein Rv0246 - *Mycobacterium tuberculosis* (strain H37RV)  
Species: *Mycobacterium tuberculosis*  
Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
Accession: B70939  
Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajamandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
*Nature* 393, 537-544, 1998  
Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
Reference number: A70500; PMID: 98295987;

AA;Accession: B70939  
AA;Status: preliminary; nucleic acid sequence not shown; translation not shown  
AA;Molecule type: DNA  
AA;Residues: 1-436 <COL>  
AA;Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA17338.1; PID  
AA;Experimental source: strain H37Rv  
CC;Genetics:  
AA;Gene: Rv0246

RESULT 5  
T20910 hypothetical protein ZK1010.9 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C;Accession: T20910; T27646  
R;McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19345  
A;Accession: T20910  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA

A;Residues: 1-635 <WIL>  
 A;Cross-references: EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN000021; CESP:ZK1010.9  
 A;Experimental source: clone F14F7  
 R;Gardner, A.  
 Submitted to the EMBL Data Library, November 1996  
 A;Reference number: Z20398  
 A;Accession: T27646  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-635 <WI2>  
 A;Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN000021; CESP:ZK1010.9  
 A;Experimental source: clone ZK1010  
 C;Genetics:  
 A;Gene: CESP:ZK1010.9  
 A;Map position: 3  
 A;Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3  
 C;Superfamily: gamma-aminobutyric acid transporter  
 Query Match 12.4%; Score 75.5%; DB 2; Length 635;  
 Best Local Similarity 36.6%; Pred. No. 11;

Matches	26 ;	Conservative	10 ;	Mismatches	28 ;	Indels	/ ;	Gaps	3 ;
QY	31	PGTAPCSRGSWSADLDKCMDCASCRARP--HSDDFCLG--CAAAPPAPERLLWPILGGAL		86					
		:     :			:	:	:		
Db	92	PTTAYKNGGLSF---LIAYVVCGLFAVPAIHMEFALGQYAAKSSPPAAFRRMMPILEGVVG							148
QY	87	SILTFVILGLLSG	97						
		:   :   :							
Db	149	WMTCVLVGAIIG	159						

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function  
A;Reference number: A690000; MUID:98037514; PMID:9371463  
A;Accession: G69099  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-261 <MTH>  
A;Cross-references: GB:AE000929; GB:AE000666; NID:92622853; PIDN:AAB86210.1; PID:92622871  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH1740  
C;Superfamily: pyruvate synthase gamma chain  
C;Keywords: coenzyme A; oxidoreductase

Query Match 12.1%; Score 73.5; DB 2; Length 261;  
Best Local Similarity 29.2%; Pred. No. 8.8;  
Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;

Qy 31 PGTAPCSRGSWSA-----DLDKCMDCASCRRA-----RPHS---DFCLGCA-AAPPAA 73  
Db 191 PGSTVKNKTKGSWRTEFKPVLDKDCIDCDNCILFCPEGGINREHEIDYDKGGGICAEKC 250

Qy 74 PFRILL 78  
Db 251 PVKAI 255

RESULT 9  
T04420 ribonuclease (EC 3.1.-.-) - barley  
C;Species: Hordeum vulgare (barley)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 22-Jun-1999  
C;Accession: T04420  
R;Rogers, J.C.; Rogers, S.W.  
Submitted to the EMBL Data Library, April 1997  
A;Reference number: Z15355  
A;Accession: T04420  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-227 <ROG>  
A;Cross-references: EMBL:AF000940; NID:92150001; PIDN:AAB58719.1; PID:92150002  
A;Experimental source: cv. Igri  
C;Genetics:  
A;Introns: 35/3; 87/3  
C;Superfamily: Enterobacter ribonuclease  
C;Keywords: hydrolase

Query Match 12.0%; Score 73; DB 2; Length 227;  
Best Local Similarity 30.0%; Pred. No. 8.8;  
Matches 30; Conservative 11; Mismatches 45; Indels 14; Gaps 4;

Qy 21 LLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGCAGAAPPAPFRLLW 79  
Db 91 LLSSRLRAEWPTLACPASDGLOFWAHREWKRKHGTCAQNLFHEHGYF---QTAAPPRPAPLLD 147

Qy 80 PIL-----GGALSLTFLVGLL---SGFLVRRRCRRERS 109  
Db 148 ALASAGVAPDGGYYTLSAVKGAIQQGTGFEPFVECNRDES 187

RESULT 10  
D75303 conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C;Accession: D75303  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F  
' M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: D75303  
A;Status: preliminary

A; Molecule type: DNA  
A; Residues: 1-346 <WHI>  
A; Cross-references: GB:AE002053; PIDN:AAFI11754.1; PIDN:g6459999; NID:g6459999; PIDN:AAFI11754.1; PIDN:g646000  
A; Experimental source: strain R1  
C; Genetics:  
A; Gene: DR2205  
A; Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;  
Best Local Similarity 28.8%; Pred. No. 13;  
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

Db 12 LLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASC---RAPHSD----FC 64  
87 LIVTCVGLGVL--TAGSASPWTV----MWVGALVAAGAVLATWHLRPAGSLFFVFA 138

Qy 65 LGCAAA--PPAFAFLWPILGALSLTFVLGILSGFLYWRRCRRERSSSPPP 113  
Db 139 VGTVGALPHPAPLPLALAVSGGAALSVALIGALGAWHSTRARPHELIAAPP 189

RESULT 11  
A55624 fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 24-Nov-2003  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Lawton, T.; Sanguineti, C.; Pereira, L.; Ramirez, J.; Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; MUID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: GB:L29454; NID:9575509; PIDN:AA56840.1; PIDN:9575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin; EGF homology F.1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;  
Best Local Similarity 25.3%; Pred. No. 75;  
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

Db 36 CSRGSSWSADDLKDMD-----CASCRAFRHS-----DFCLGC 67  
2040 CPEGFSWSSGRQRCDLRLMSYCAYKEGGKCCALKQECCCCSKQEPKSRNHS 2099

Qy 68 AAAPPAPFLWPILGAL 86  
Db 2100 PTEPDEAFRQICPGSGII 2118

RESULT 12  
T36798 Probable transcription regulator soxR-like - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
C;Accession: T36798  
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
Submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21614  
A;Accession: T36798  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-175 <OLI>  
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18C  
A;Experimental source: strain A3 (2)  
C;Genetics:  
A;Gene: SCOEDB:SCI30A.18C

Query Match 11.7%; Score 71; DB 2; Length 175;

A; Reference number: JC1281; MUID: 93038690; PMID: 1417860  
 A; Accession: JC1281  
 A; Molecule type: mRNA  
 A; Residues: 1-20, 'T', 22-311, 'Y', 313-361, 'A', 363-514, 'I', 516-558 <KAR>  
 A; Cross-references: GB:L02896; NID:9204424; PID:AAA86439.1; PID:g204425  
 A; Experimental source: brain  
 A; Accession: PC1132  
 A; Molecule type: protein  
 A; Residues: 24-55; 424-445 <KA2>  
 C; Superfamily: Glypican  
 C; Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; heparan  
 E; 1-23/Domain: signal sequence #status predicted <SIG>  
 E; 24-530/Product: glypican #status predicted <MAT>  
 F; 531-558/Domain: carboxyl-terminal propeptide #status predicted <CRP>  
 F; 55, 488, 490/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
 F; 79, 116/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 399, 512/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F; 530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query	Match	Score	DB	Length
	Best Local Similarity	11.5%	2	558;
Db	Matches 26; Conservative	37.7%	Pred. No.	33;
		6;	Mismatches	19;
			Indels	18;
			Gaps	5;

Qy	11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCR----ARPHSDFC 64
Db	221 RSEFVQGLGVASDWVRKVA--QVPLAPECSRA-----VMKLVYCAHCRGVPGARPCPDYC 272

Qy	65 ----LGCAA 69
Db	273 RNTLKGCLA 281

**RESULT 15**  
 D#5330  
 probable beta-lactamase - Deinococcus radiodurans (strain R1)  
 C; Species: Deinococcus radiodurans  
 C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C; Accession: D75330  
 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A; Reference number: A75250; MUID: 20036896; PMID: 10567266  
 A; Accession: D75330  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-424 <WHI>  
 A; Cross-references: GB:AE002036; GB:AE000513; NID:96459766; PID:AAFF11537.1; PID:g645977  
 A; Experimental source: strain R1  
 C; Genetics:  
 A; Gene: DR1985  
 A; Map position: 1

Query	Match	Score	DB	Length
	Best Local Similarity	11.4%	2	424;
Db	Matches 30; Conservative	29.7%	Pred. No.	30;
		11;	Mismatches	35;
			Indels	25;
			Gaps	4;

Qy	3 RGSLRLRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRA----- 57
Db	2 RGFIRTLTLALLLG---AGINACRNREAQDTAPPAAAQSQAAPRKAAASSSPAPTATE 58

Qy	58 ---RPHSDFCLGCAA-----PPAPFRLWPILGGALSL 88
Db	59 PAVSAPAADGCLPAAPAVTQAPRPPQP-----LSGRIGL 92

Search completed: March 1, 2004, 16:44:47  
 Job time : 43 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
<b>SUMMARIES</b>							
-	-	-	-	-	-	-	-
1	571	93.9	129	1	FN14_HUMAN	Q9npB4	homo sapien
2	445	73.2	129	1	FN14_MOUSE	Q9cr75	m tumor nec
3	87	14.3	184	1	T13C_HUMAN	Q96rj3	homo sapien
4	78	12.8	448	1	FBL5_RAT	Q9vh8	rattus norv
5	77	12.7	448	1	FBL5_MOUSE	Q9vh9	mus musculu
6	76.5	12.6	245	1	FLIP_SALTY	P54706	salmonella
7	74	12.2	548	1	LGI3_MOUSE	Q8k406	mus musculu
8	73.5	12.1	81	1	PORD_METTH	P56815	methanobact
9	72	11.8	1278	1	NPC1_HUMAN	Q15118	homo sapien
10	72	11.8	2871	1	FBN1_MOUSE	Q61554	mus musculu
11	70	11.5	301	1	CTF5_HUMAN	Q9ujaz2	homo sapien
12	70	11.5	443	1	FBL4_MOUSE	Q9wvj9	mus musculu
13	70	11.5	558	1	GPCI_RAT	P35053	rattus norv
14	69.5	11.4	495	1	MLP2_DRONE	Q24400	drosophila
15	69	11.3	180	1	PTTG_HUMAN	P53801	homo sapien
16	69	11.3	314	1	TRI2_HUMAN	Q14140	homo sapien
17	69	11.3	324	1	TNR6_RAT	Q63199	rattus norv
18	68.5	11.3	205	1	GSCL_HUMAN	Q15499	homo sapien
19	68.5	11.3	431	1	YGB4_METTH	Q27719	methanobact
20	67.5	11.1	368	1	GP62_HUMAN	Q9bzj7	homo sapien
21	67.5	11.1	1008	1	VGLM_UK	P09613	uukuniemi
22	67.5	11.1	1013	1	EPAS_CHICK	P54755	gallus gall
23	67	11.0	279	1	CXE1_HUMAN	Q8nfk1	homo sapien
24	67	11.0	319	1	BST1_RAT	Q63072	rattus norv
25	67	11.0	386	1	HXAD_MOUSE	Q62424	mus musculu
26	67	11.0	1005	1	EPA5_RAT	P54757	rattus norv
27	67	11.0	2871	1	FBNL_PIG	Q9tv36	sus scrofa
28	66.5	10.9	443	1	FBL4_CRIGR	Q50508	cricetus
29	66	10.9	394	1	Y6B9_PSEAE	P42514	pseudomonas
30	66	10.9	992	1	POLS_RUBVM	P08563	rubella vir
31	66	10.9	1238	1	JAG2_HUMAN	Q9y219	homo sapien
32	66	10.9	2318	1	NTC3_MOUSE	Q61982	mus musculu
33	66	10.9	2319	1	NTC3_RAT	Q9r172	rattus norv

Scoring table: ELOSUM62  
 Sequence: 1 MARGSLRRRLRLVGLWLA.....LSGFLWWRCCRERSSPPPX 114  
 Perfect score: 608  
 Title: US-10-062-599-59

Scoring table: Gapop 10.0 , Gapext 0.5  
 Searched: 141681 seqs, 52070155 residues  
 Total number of hits satisfying chosen parameters: 141681  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1							
FN14_HUMAN							
ID	FN14_HUMAN	STANDARD;	PRT;	129 AA.			
AC	Q9NPB4; Q9HCS0;						
DT	28-FEB-2003 (Rel. 41, Created)						
DT	28-FEB-2003 (Rel. 41, Last sequence update)						
DT	10-OCT-2003 (Rel. 42, Last annotation update)						
DE	Tumor necrosis factor receptor superfamily member Fn14 precursor						
DE	(Fibroblast growth factor-inducible immediate-early response protein 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).						
DE	TNFRSF12A OR FN14.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
[1]	SEQUENCE FROM N.A. (ISOFORM 1).						
RC	TISSUE=Placenta;						
RX	MEDLINE=20216634; PubMed=10751351;						
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W., Testa J.R., Peifley K.A., Winkles J.A.;						
RA	"The Fn14 immediate-early response gene is induced during liver regeneration and highly expressed in both human and murine hepatocellular carcinoma.";						
RA	Tanaka S., Sugimachi K.;						
RA	"Human homologue of Fn14.";						
RL	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.						
[2]	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).						
RT	SEQUENCE FROM N.A. (ISOFORM 2).						
RT	Am. J. Pathol. 156:1253-1261 (2000).						
RN	[2]						
RC	SEQUENCE FROM N.A. (ISOFORM 1).						
RX	TISSUE=Uterus;						
RA	MEDLINE=22388257; PubMed=12477932;						
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Sherman C.M., Schaefer C.F., Bhat N.K., Hopkins R.D., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [4] FUNCTION.						
RA	[3]						
RP							

RX MEDLINE=21585797; PubMed=11728344;  
 RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,  
 RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;  
 RT "A novel TNF receptor family member binds TWEAK and is implicated in  
 angiogenesis.";  
 RL Immunity 15: 837-846 (2001).  
 CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in  
 some cell types. Promotes angiogenesis and the proliferation of  
 endothelial cells. May modulate cellular adhesion to matrix  
 proteins.  
 CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
 TRAF3.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC -!- Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9NPB4-1; Sequence=Displayed;

CC Name=2;  
 CC IsoId=Q9NPB4-2; Sequence=VSP\_006519;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and  
 kidney. Intermediate expression in lung, skeletal muscle and  
 pancreas.  
 CC -!- INDUCTION: BY FGF-1 and phorbol ester.  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AF191148; AAF69108.1; -.  
 DR EMBL; AB035480; BAA94792.1; -.  
 DR EMBL; AB035481; BAB17850.1; -.  
 DR Genbank; BC002718; AAH02718.1; -.  
 DR Genbank; HGNC:18152; TNFRSF12A.  
 DR MIN; 605914; -.  
 DR GO; GO:0006928; P:cell motility; TAS.  
 DR GO; GO:0007275; P:development; TAS.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
 DR Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;  
 KW Alternative splicing.  
 FT SIGNAL\_1 27 POTENTIAL.  
 FT CHAIN 28 129 TUMOR NECROSIS FACTOR RECEPTOR  
 SUPERFAMILY MEMBER FN14.  
 FT DOMAIN 28 80 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 81 101 POTENTIAL.  
 FT DOMAIN 102 129 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 36 67 TNFR-CYS (ATYPICAL).  
 FT DISULFID 36 49 POTENTIAL.  
 FT DISULFID 52 67 POTENTIAL.  
 FT VARSPlic 33 67 Missing (in isoform 2).  
 /FTId=VSP\_006519.

SQ SEQUENCE 129 AA; 13911 MW; BF3EDFB9C1E1C448 CRC64;

Query Match 93.9%; Score 571; DB 1; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 2.8e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLALLRSVAGEQAPGTAPCSRGGSSWASADLDKCMDCACSCRAPH 60  
 Db 1 MARGSLRLLRLVLLGLWLALLRSVAGEQAPGTAPCSRGGSSWASADLDKCMDCACSCRAPH 60

61 SDFCLGCAAAPPAPAPFLWLPILGGAALSLTFVLGLLSGFLYWRRCRRERSSPPP 113  
 61 SDFCLGCAAAPPAPFLWLPILGGAALSLTFVLGLLSGFLYWRRCRRERKFTTP 113

FN14\_MOUSE STANDARD; PRT; 129 AA.  
 ID FN14 MOUSE Q9ZQW3;  
 AC Q9CR75; Q9ZQW3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
 DE (Fibroblast growth factor-inducible immediate-early response protein  
 DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)  
 DE (Tweak-receptor) (TweakR).  
 GN TNFRSF12A OR FN14 OR FGFRP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1] RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Fibroblast;  
 RX MEDLINE=20020297; PubMed=10551889;  
 RA Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,  
 RA Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Richards C.M., Winkles J.A.;  
 RT "The mitogen-inducible Fn14 gene encodes a type I transmembrane  
 protein that modulates fibroblast adhesion and migration.";  
 RT J. Biol. Chem. 274:33166-33176 (1999).  
 RL [2] RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyoo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3] RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Grouse L.H., Derge J.G.,  
 RA Klaushner R.D., Collins F.S., Wagner L., Sheenmen C.M., Schulter G.D.,  
 RA Altschul S.F., Zeeberg B., Buettner K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalob D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marr M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Receptor for TNFSF12/TWEAK (By similarity). Weak inducer of apoptosis in some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion to matrix proteins.

CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with TRAF3 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine, kidney, liver, lung and skin, and in adult heart and ovary.

CC Intermediate expression in adult kidney, lung and skin.

CC -!- INDUCTION: By FGF-1.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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DR EMBL; AF156164; AAF07882.1; -.

DR EMBL; AK005530; BAB24101.1; -.

DR EMBL; AK005382; BAB23989.1; -.

DR EMBL; BC025860; AAH25860.1; -.

DR MGD; MGI:1351484; Tnfrsf12a.

DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR GO; GO:0006931; P:substrate-bound cell migration, cell attach. . . ; IDA.

DR InterPro; IPR001368; TNFR\_c6.

DR PROSITE; PS006552; TNFR\_NGFR\_1; FALSE NEG.

DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE NEG.

KW Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal.

FY SIGNAL 1 27 POTENTIAL.

FT CHAIN 28 129 TUMOR NECROSIS FACTOR RECEPTOR

FT DOMAIN 28 80 SUPERFAMILY MEMBER FN14.

FT TRANSMEM 81 101 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 102 129 POTENTIAL.

FT REPEAT 36 67 CYTOPLASMIC (POTENTIAL).

FT DISULFID 36 49 TNFR-CYS (ATYPICAL).

FT DISULFID 52 67 POTENTIAL.

FT CONFLICT 3 4 SA -> PG (IN REF. 1).

SQ SEQUENCE 1.29 AA; 13641 MW; 1665C68B4D9A9253 CRC64;

Query Match 73.2%; Score 445; DB 1; Length 129;

Best Local Similarity 74.3%; Pred. No. 3.6e-36;

Matches 84; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLRLVGLWLALLRSVAQEAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Db 1 MASAWPRSLPQIQLVGLFGLVLMRAAAAGEQAPGTPSPCSSGSSWSADLDKCMDCASCPAPRH 60

QY 61 SDRCLGCAAAPPAPERLLWPILGGNLSLTFVLGLISGFLWRRCRRESSPPP 113

Db 61 SDRCLGCAAAPPAPERLLWPILGGNLSLVLTALVSSFLWRRCRREKFTTP 113

RESULT 3

T13C\_HUMAN STANDARD; PRT; 184 AA.

AC Q96RJ3;

AC Q96RJ3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor)

DE 3).

GN TNFRSF13C OR BAFF OR BR3.

OS Homo sapiens (Human).

OC Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

[1]

RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RP TISSUE=B-cell lymphoma; MEDLINE=21442025; PubMed=11509692;

RC Thompson J.S., Bixlers S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C., Strauch K., Zafari M., Benjamin C.D., Tschoopp J., Browning J.L., Ambrose C.; "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF.";

RA RT with BAFF.";

RA Science 293:2108-2111(2001).

RL RN [2]

RP FUNCTION.

RX MEDLINE=21475520; PubMed=11591325;

RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;

RA "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";

RT Curr. Biol. 11:1547-1552(2001).

RL -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS.

CC Promotes the survival of mature B-cells and the B-cell response.

CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q96RJ3-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q96RJ3-2; Sequence=VSP\_006505;

CC Note=No experimental confirmation available;

CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and in resting B-cells. Detected at lower levels in activated B-cells, resting CD4+ T-cells, in thymus and peripheral blood leukocytes.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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CC EMBL; AF373846; AAK91826.1; -.

CC DR; IMPV; 30-OCT-02.

CC DR; HGNC:17755; TNFRSF13C.

CC DR; 606269; -.

CC DR; InterPro; IPR001368; TNFR\_c6.

CC DR; PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.

CC DR; PROSITE; PS50050; TNFR\_NGFR\_2; FALSE NEG.

CC DR; Receptor; Immune response; Signal-anchor; Transmembrane;

CC DR; Alternative splicing; 3D-structure.

CC DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).

CC FT TRANSMEM 79 99 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN) (POTENTIAL).

CC FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).

CC FT REPEAT 18 35 BY SIMILARITY.

CC FT DISULFID 19 32 BY SIMILARITY.

CC FT DISULFID 24 35 BY SIMILARITY.

CC FT VARSPLIC 143 143 P -> PA (in isoform 2).

CC FT /FTId=VSP\_006505.

CC SQ SEQUENCE 184 AA; 18863 MW; F2BF89B099A27138 CRC64;

Query Match 14.3%; Score 87; DB 1; Length 184;

Best Local Similarity 27.0%; Pred. No. 0.13;

Matches 34; Conservative 11; Mismatches 41; Indels 40; Gaps 6;

QY 23 RSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Db 6 RSLRGDAPAPTPCVPAECFDLVRHCAGGLIRTPRPKP----AGASSPAPRTAQPO 60

QY 81 -----ILGGA---LSLTFVGLG-LSGFLVWRCCR-----E 107

Db 61 ESVGAGAGEAALPLPGLLFGAPALLGLAVLVGLVSWRQRRLRGASSAEAPDGD 120

QY 108 RSSPPP 113  
: : |  
DB 121 KDAPEP 126

**RESULT 4**  
**FBL5\_RAT** STANDARD; PRT; 448 AA.  
AC Q9WVH8; Q9R284;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibulin-5 Precursor (FBL5-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (EVBC).  
DE FBLN5 OR DANCE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
MEDLINE=99357779; PubMed=10428823;  
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M., Olson E.N.;  
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;  
RT "DANCE, a novel secreted RGD protein expressed in developing, atherosclerotic, and balloon-injured arteries.";  
RL J. Biol. Chem. 274:22476-22483 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
MEDLINE=99278197; PubMed=10347091;  
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;  
RT "EVBC, a novel epidermal growth factor-like repeat-containing protein upregulated in embryonic and diseased adult vasculature.";  
RL Circ. Res. 84:1166-1176 (1999).  
CC FUNCTION: Promotes adhesion of endothelial cells through interaction of integrins and the RGD motif. Could be a vascular ligand for integrin receptors and may play a role in vascular development and remodeling.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the fibulin family.  
CC -!- SIMILARITY: Contains 6 EGF-like domains.

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CC EMBL; AF112153; ADD41769.1; -.  
DR EMBL; AF137350; ADD25101.1; -.  
DR HSSP; P00736; 1APQ.  
DR InterPro; IPR000152; ASX\_hydroxyl\_S.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_1.  
DR Pfam; PF00008; EGF\_4.  
DR SMART; SM00179; EGF\_Ca; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS50026; EGF\_3; 5.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain; Glycoprotein.  
FT SIGNAL. 1 23 POTENTIAL.  
FT CHAIN 24 448 FIBULIN-5.  
FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.  
FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 298 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
FT SITE 54 56 CELL\_ATTACHMENT SITE (POTENTIAL).  
FT DISULFID 131 144 BY SIMILARITY.  
FT DISULFID 138 153 BY SIMILARITY.  
FT DISULFID 155 166 BY SIMILARITY.  
FT DISULFID 172 181 BY SIMILARITY.  
FT DISULFID 177 190 BY SIMILARITY.  
FT DISULFID 192 205 BY SIMILARITY.  
FT DISULFID 211 221 BY SIMILARITY.  
FT DISULFID 217 230 BY SIMILARITY.  
FT DISULFID 232 245 BY SIMILARITY.  
FT DISULFID 251 262 BY SIMILARITY.  
FT DISULFID 258 271 BY SIMILARITY.  
FT DISULFID 273 286 BY SIMILARITY.  
FT DISULFID 292 305 BY SIMILARITY.  
FT DISULFID 299 314 BY SIMILARITY.  
FT DISULFID 320 332 BY SIMILARITY.  
FT CARBOHYD 283 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 238 238 L -> P (IN REF. 2).  
SQ SEQUENCE 448 AA; 50160 MW; E6BC68F7BF14B714 CRC64;  
Query Match 12.8%; Score 78; DB 1; Length 448;  
Best Local Similarity 24.1%; Pred. No. 2.2;  
Matches 26; Conservative 8; Mismatches 24; Indels 50; Gaps 5;  
QY 6 LRRLLRLVGLWLALLRSVAGEQAPGTA--PCSRGSSWSADDKCMDASCARPHSDF 63  
|:|:|:|||:|||:|||:|||:|||:  
Db 4 LKRILTVTILAIWL-----PHPGNAQQQCTNGFDLDQTGQCLDIDECRTIPEA-- 52  
QY 64 CLG------C-----AAAPPAP 74  
Db 53 CRGDDMMCVQNQNGGYLCIPRTNPVYRGPYNSNPYSTYSGPYPAAAPPVP 100

**RESULT 5**  
**FBL5\_MOUSE** STANDARD; PRT; 448 AA.  
ID FBL5\_MOUSE  
AC Q9WVH9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE FBLN5 precursor (FBL5-5) (Developmental arteries and neural crest EGFR-like protein) (Dance).  
GN FBLN5 OR DANCE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9357779; PubMed=10428823;  
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M., Olson E.N.;  
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;  
RT "DANCE, a novel secreted RGD protein expressed in developing, atherosclerotic, and balloon-injured arteries.";  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; RT	Matches 26; Conservative 8; Mismatches 24; Indels 50; Gaps 5;
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";	6 LRRRLRLVGLWALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRARPHSDF 63
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	4 LKRILTVTILALWL-----PHPGNAQQQCTNGFDLDRQSGQCLDDECRTIPEA-- 52
RA	-!- FUNCTION: Promotes adhesion of endothelial cells through interaction of integrins and the RGD motif. Could be a vascular ligand for integrin receptors and may play a role in vascular development and remodeling.	64 CLG-----C-----AAAPPAP 74
CC	-!- SUBCELLULAR LOCATION: Secreted.	53 CRGDMMCYVNONGGYLCIPRTNPVYRGPSNPNYSTSYGSPYPAAPVP 100
CC	-!- SIMILARITY: Belongs to the fibulin family.	RESULT 6
CC	-!- SIMILARITY: Contains 6 EGF-like domains.	FLIP SALTY STANDARD; PRT; 245 AA.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ) or send an email to license@isb-sib.ch).	AC P54700; ID FLIP SALTY STANDARD; PRT; 245 AA.
CC	DR EMBL; AF112151; AAD41767.1; .	DT 01-OCT-1996 (Rel. 34, Created)
CC	DR EMBL; BC006636; AAH06636.1; .	DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC	DR HSSP; P00736; LAPQ.	DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC	DR MGD; MGI:1346091; Fbln5.	DE FLIP OR FLAR OR STM1979.
CC	DR InterPro; IPR000152; Abx_hydroxyl_S.	GN OS Salmonella typhimurium.
CC	DR InterPro; IPR001881; EGF_Ca.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
CC	DR InterPro; IPR006209; EGF_Like.	[1] NCBI_TaxID=602;
CC	DR PFAM; PF0008; EGF; 4.	RN [2]
CC	DR SMART; SM00179; EGF; 4.	SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
CC	DR PROSITE; PS00010; ASX_HYDROXYL; 4: .	RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
CC	DR PROSITE; PS00022; EGF_1; FALSE_NEG.	RX MEDLINE=97464436; PubMed=9324257;
CC	DR PROSITE; PS01186; EGF_2; 4: .	RA Ohnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab R.M.;
CC	DR PROSITE; PS50026; EGF_3; 5: .	RT "The FlIO, FlIP, FlIQ, and FlR proteins of <i>Salmonella typhimurium</i> : putative components for flagellar assembly.";
CC	DR PROSITE; PS01187; EGF_CA; 6: .	RT J. Bacteriol. 179:6092-6099(1997).
CC	KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain; Glycoprotein.	RL RN
FT	SIGNAL 1 23	RP SEQUENCE FROM N.A.
FT	CHAIN 24 448	RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
FT	DOMAIN 24 69	RX MEDLINE=21534948; PubMed=11677609;
FT	DOMAIN 127 167	RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
FT	DOMAIN 168 206	RA "Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2.";
FT	DOMAIN 207 246	RN Nature 413:852-856 (2001).
FT	DOMAIN 247 287	RT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
FT	DOMAIN 288 333	CC -!- FUNCTION: Plays a role in the flagellum-specific transport system (By similarity).
FT	SITE 54 56	CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
FT	DISULFID 131 144	CC -!- MISCELLANEOUS: For insertion of FlIP into the membrane, cleavage of the signal peptide is important kinetically but not absolutely required.
FT	DISULFID 24 448	CC -!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC
FT	DISULFID 54 56	CC
FT	DISULFID 131 144	CC
FT	DISULFID 24 448	CC
FT	DISULFID 24 69	CC
FT	DISULFID 127 167	CC
FT	DISULFID 168 206	CC
FT	DISULFID 207 246	CC
FT	DISULFID 247 287	CC
FT	DISULFID 288 333	CC</

KW Protein transport; Signal; Complete proteome.

FT SIGNAL 1 21 FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.

FT CHAIN 22 245 POTENTIAL.

FT TRANSMEM 45 65 POTENTIAL.

FT TRANSMEM 88 108 POTENTIAL.

FT TRANSMEM 185 205 POTENTIAL.

FT TRANSMEM 209 229 POTENTIAL.

SQ SEQUENCE 245 AA; 26787 MW; C9A4241F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 1; Length 245;

Best Local Similarity 30.8%; Pred. No. 1.8;

Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRLRLRLVGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59

:| | | :| | | :| | | :| | | :| | | :| | |

Do 1 MRRLLFLSILAGLW--LFSPEAAAQLPGLISQPLAGGGQSWSLSQLVFTSLTFLPAI 58

QY 60 -HSDF-----CLGCAAAAPPAPERLWPILGGAISITFVL 92

:| | | :| | | :| | | :| | |

Dd 59 LMMSFTRILLIVFGLLRNALGTSPSAPPNQV----LIGLALFLTEFI 100

RESULT 7

LGI13\_MOUSE STANDARD; PRT; 548 AA.

ID LGI13\_MOUSE STANDARD; PRT; 548 AA.

AC Q8K406;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Leucine-rich repeat LGI family member 3 precursor (Leucine-rich glioma-inactivated protein 3) (Leubrin).

GN LGI13.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Brain;

RA Yun H.-Y., Lee S.E.;

RT Submitted' (NOV-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Hippocampus;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto K., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultan R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shinagawa A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashiaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573 (2002).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J.M., Marras M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL CC !- SUBCELLULAR LOCATION: Secreted (Potential).

CC !- SIMILARITY: Contains 6 EAR repeats.

CC !- SIMILARITY: Contains 5 Leucine-rich (LRR) repeats.

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CC DR AF515590; AAM55219.1; EMBL; AY174077; AAO19739.1; DR EMBL; AK049831; BAC33943.1; DR EMBL; BC055315; AAH55315.1; DR EMBL; BC061460; AAH61460.1; DR MGD; MGI:2182619; Lgi3. DR InterPro; IPR009039; EAR. DR InterPro; IPR005492; EPTP. DR InterPro; IPR001611; LRR. DR InterPro; IPR000483; LRR\_Cterm. DR InterPro; IPR003591; LRR\_typ. DR Pfam; PF03736; EPTP; 2. DR Pfam; PF00560; LRR; 3. DR Pfam; PF01463; LRRCT; 1. DR SMART; SM00369; LRR\_TYP; 3. DR SMART; SM00082; LRR2; DR PROSITE; PS50912; EAR; 6. DR Repeat; Leucine-rich repeat; Signal. DR SIGNAL 1 30 LEUCINE-RICH REPEAT LGI FAMILY MEMBER 3. CHAIN 31 548 LRR 1. FT REPEAT 63 86 LRR 2. FT REPEAT 87 110 LRR 3. FT REPEAT 112 134 LRR 4. FT REPEAT 135 158 LRR 5. FT REPEAT 160 183 LRR 6. FT REPEAT 221 264 EAR 1. FT REPEAT 267 310 EAR 2. FT REPEAT 313 361 EAR 3. FT REPEAT 362 406 EAR 4. FT REPEAT 409 453 EAR 5. FT REPEAT 454 497 EAR 6. FT CARBOHYD 189 N-LINKED (GLCNAC. . . ) (POTENTIAL). FT CARBOHYD 311 N-LINKED (GLCNAC. . . ) (POTENTIAL). SQ SEQUENCE 548 AA; 61817 MW; 2DB303936354B958 CRC64;

Query Match

Best Local Similarity 40.4%; Pred. No. 6.4;  
 Matches 21; Conservative 5; Missmatches 24; Indels 2; Gaps 1;

QY 3 RGSLRRRLRLVGLWALLRSVAGEQQAPGTAPCSRGSWSADLDKXMDCAS 54  
 DB 8 RGPGRLLVLSTLGFCLML--QVSAKRPPKTPPPCPPSCSCTRDTAFCVDSKS 57

## RESULT 8

PORD\_METTH STANDARD; PRT; 81 AA.

AC P56815;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).  
 GN PORD OR MTH1 740.1.  
 OS Methanobacterium thermoautotrophicum.  
 Archaea, Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter. NCBI\_TaxID=187420;  
 OX [1]  
 RN PSEQUENCE FROM N.A.  
 RC STRAIN=Delta H;  
 RX MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Batwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";  
 RT J. Bacteriol. 179:7135-7155 (1997).  
 -: CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-CoA + CO (2) + reduced ferredoxin.  
 CC -: COFACTOR: Binds 2 4Fe-4S clusters.  
 CC -: SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one gamma chain.  
 CC -: SIMILARITY: Belongs to the bacterial-type ferredoxin family.  
 CC -: CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.

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EMBL; AE000929; AAB86210.1; ALT\_INRT.  
 DR HSSP; P00195; ICLF.  
 DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
 DR Pfam; PF00037; fer4; 2.  
 DR PROSITE; PS00198; 4E4S\_FERREDOXIN; 2.  
 KW Oxidoreductase; Electron\_transport; Iron-sulfur; Repeat; 4Fe-4S;  
 KW Complete proteome.

FT METAL 34 34 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).  
 FT METAL 37 37 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).  
 FT METAL 40 40 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).  
 FT METAL 44 44 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).  
 FT METAL 60 60 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).  
 FT METAL 63 63 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).  
 FT METAL 66 66 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).  
 FT METAL 70 70 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).  
 SQ SEQUENCE 81 AA; 9121 MW; 219A9CCAE8A41604 CRC64;

Query Match 12.1%; Score 73.5%; DB 1; Length 81;  
 Best Local Similarity 29.2%; Pred. No. 1.2;  
 Matches 19; Conservative 8; Missmatches 21; Indels 17; Gaps 4;

QY 31 PGTAPCSRGSWSA----DLDKCMDASCRA----RPHS---DFCLGCA-AAPBA 73  
 DB 11 PGSTVCKNTGWSWRTEFKPVLDKDCKIDCDNCILFCPEGGINREHEIDYDCKGGCGICAERKC 70  
 QY 74 PERLL 78  
 DB 71 PVKAI 75

## RESULT 9

NPC1\_HUMAN STANDARD; PRT; 1278 AA.

ID NPC1\_HUMAN ID O15118; Q9P130;  
 AC 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Niemann-Pick C1 protein precursor.  
 GN NPC1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;  
 RN [1] RP SEQUENCE FROM N.A., AND VARIANTS NPC1.  
 RX MEDLINE=97362323; PubMed=9211849;  
 RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D., Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B., Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A., Higgins M.E., Comly M., Cooney A., Brown A., Kanetsky C.R., Blanchette-Mackie E.J., Neufeld E.B., Chang T.-Y., Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J., Markie D., O'Neill R.R., van Diggelen O.P., Ellender M., Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.; RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol homeostasis"; RT Science 277:228-231 (1997).  
 RL [2] RP SEQUENCE FROM N.A., AND VARIANTS NPC1.  
 RX MEDLINE=99355599; PubMed=10425213;  
 RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G., Carstea E.D.; RT "The genomic organization and polymorphism analysis of the human Niemann-Pick C1 gene."; RT Biochem. Biophys. Res. Commun. 261:493-498 (1999).  
 RL [3] RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623216; PubMed=11754101;  
 RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J., Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.; RT "NPC1: Complete genomic sequence, mutation analysis, and characterization of haplotypes."; RT Hum. Mutat. 19:30-38 (2002).  
 RL [4] RP CHARACTERIZATION.  
 RX MEDLINE=99128318; PubMed=9927649;  
 RA Watari H., Blachette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S., Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III; RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and lysosomal targeting in cholesterol mobilization."; RT Proc. Natl. Acad. Sci. U.S.A. 96:805-810 (1999).  
 RL [5] RP VARIANT NPD TRP-992.  
 RX MEDLINE=98299797; PubMed=9634529;  
 RA Greer W.L., Riddell D.C., Gillian T.L., Giroudard G.S., Sparrow S.M., Byers D.M., Dobson M.J., Neumann P.E.; RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a G3097-->T transversion in NPC1."; RT Am. J. Hum. Genet. 63:52-54 (1998).  
 RL [6] RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; TRP-992; ALA-1007;  
 RP THR-1061 AND VAL-1213.  
 RX MEDLINE=99452586; PubMed=10521290;

Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C., Neumann P.E.; "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich domain."; Am. J. Hum. Genet. 65:1252-1260(1999).

[7] VARIANT NPC1 THR-1061.  
MEDLINE=9452593; PubMed=10521297;

RX RA Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A., Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.; RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant allele in patients of Western European descent and correlates with a classic juvenile phenotype.";  
RT RIL Am. J. Hum. Genet. 65:1321-1329(1999).

RN [8] VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.  
RP MEDLINE=9408226; PubMed=10480349;

RX RA Yamaoka T., Nanba E., Ninomiya H., Higaki K., Taniuchi M., Zhang H., Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A., Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G., Ohno K.; RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease type C.";  
RT RIL Hum. Genet. 105:10-16(1999).

RN [9] VARIANTS NPC1 GLN-958 AND ALA-1007.  
RP MEDLINE=21313105; PubMed=11349231;

RX RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F., Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.; RT "Niemann-Pick C variant detection by altered sphingolipid trafficking and correlation with mutations within a specific domain of NPC1.";  
RT RIL Am. J. Hum. Genet. 68:1361-1372(2001).

RN [10] VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.  
RP MEDLINE=21313105; PubMed=11333381;

RX RA Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K., Wenger D.A., Ohno K., Vanier M.T.;

RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels of NPC1 protein, and phenotypes emphasize the functional significance of the putative sterol-sensing domain and of the cysteine-rich luminal loop.";  
RT RIL Am. J. Hum. Genet. 68:1373-1385(2001).

RN [11] VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.  
RP MEDLINE=21372069; PubMed=11479732;

RX RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T., Millat G.; RT "Niemann-Pick type C disease: NPC1 mutations associated with severe and mild cellular cholesterol trafficking alterations.";  
RT RIL Hum. Genet. 109:24-32(2001).

-!- FUNCTION: Involved in the intracellular trafficking of cholesterol. May play a role in vesicular trafficking in glia, a process that may be crucial for maintaining the structural and functional integrity of nerve terminals.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late endosomes and lysosomes.

-!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain containing a di-leucine motif necessary for lysosomal targeting are critical for mobilization of cholesterol from lysosomes.

-!- PTM: Glycosylated.

-!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid storage disorder, which affects particularly the brain, liver and spleen, and which is characterized by lysosomal accumulation of low density lipoprotein derived cholesterol. Clinical features include variable hepatosplenomegaly and severe progressive neurological dysfunction such as ataxia, dystonia and dementia. The age of onset can vary from infancy to late adulthood.

-!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease type D (NPD) [MIM:257250]; also known as Niemann-Pick disease without sphingomyelinase deficiency, or Nova Scotian type. Because of evidence from biochemical changes, lack of complementation, and linkage mapping to the same chromosome site, NPD and NPC1 are

considered to be allelic disorders.

CC -!- SIMILARITY: Belongs to the patched family.

CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.

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CC EMBL; AF002020; AAB63982.1; -.

DR EMBL; AF157379; AAD48006.1; -.

DR EMBL; AF157365; AAD48006.1; JOINED.

DR EMBL; AF157366; AAD48006.1; JOINED.

DR EMBL; AF157367; AAD48006.1; JOINED.

DR EMBL; AF157368; AAD48006.1; JOINED.

DR EMBL; AF157369; AAD48006.1; JOINED.

DR EMBL; AF157370; AAD48006.1; JOINED.

DR EMBL; AF157371; AAD48006.1; JOINED.

DR EMBL; AF157372; AAD48006.1; JOINED.

DR EMBL; AF157373; AAD48006.1; JOINED.

DR EMBL; AF157374; AAD48006.1; JOINED.

DR EMBL; AF157375; AAD48006.1; JOINED.

DR EMBL; AF157376; AAD48006.1; JOINED.

DR EMBL; AF157377; AAD48006.1; JOINED.

DR EMBL; AF157378; AAD48006.1; JOINED.

DR EMBL; AF338230; AAK25791.1; -.

DR EMBL; AF123046; AAF28875.1; -.

DR EMBL; AF123045; AAF28875.1; JOINED.

DR Genew; HGNC:7897; NPC1.

DR MIM; 607623; -.

DR MIM; 257220; -.

DR MIM; 257250; -.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0005764; C:lysosome; TAS.

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0005478; F:intracellular transporter activity; TAS.

DR GO; GO:0015248; F:sterol transporter activity; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

DR InterPro; IPR004765; NP\_C type.

DR InterPro; IPR003392; Patched.

DR InterPro; IPR000731; SSD\_5TM.

DR Pfam; PF02460; Patched; 1.

DR TIGRFAMS; TIGR00917; 2A060601; 1.

DR PROSITE; PS50156; SSD; 1.

KW Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism; Disease mutation.

KW SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 1278 NIEMANN-PICK C1 PROTEIN.

FT TRANSMEM 270 290 POTENTIAL.

FT TRANSMEM 351 371 POTENTIAL.

FT TRANSMEM 622 642 POTENTIAL.

FT TRANSMEM 655 675 POTENTIAL.

FT TRANSMEM 678 698 POTENTIAL.

FT TRANSMEM 760 780 POTENTIAL.

FT TRANSMEM 833 853 POTENTIAL.

FT TRANSMEM 1099 1119 POTENTIAL.

FT TRANSMEM 1125 1145 POTENTIAL.

FT TRANSMEM 1196 1216 POTENTIAL.

FT TRANSMEM 1228 1248 POLY-PRO.

FT DOMAIN 249 259 POTENTIAL.

FT DOMAIN 620 785 SSD.

FT SITE 1275 1278 DI-LEUCINE MOTIF.

FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 11.8%; Score 72; DB 1; Length 1278;

Best Local Similarity 31.4%; Pred. No. 22;

Matches 27; Conservative 8; Mismatches 17; Indels 34; Gaps 7;

Qy 33 TAPCSRGSWSAADDKOMDCA-SCRAPHSDFCLGCCRAAPPAPFRLLWPIIG----GAI 86

Db 235 TAPCS-----CQDCSIVCGPKPQ-----PPPPAP----WTLGLDAMYVIM 272  
 QY 87 SLTFVLGIL----SGFLYWRRCRRER 108  
 :|::|:|:|:|:|:  
 Db 273 WITYMAFLVFFGAFFAVW--CYRKRR 296

**RESULT 1.0**

**FBN1\_MOUSE STANDARD; PRT; 2871 AA.**

ID FBN1\_MOUSE STANDARD; PRT; 2871 AA.  
 AC O61554; Q60826;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBN1 OR FBN-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95130561; PubMed=7829516;  
 RA Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T., Pereira L., Ramirez F., Bonadio J.;  
 RA "Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene.";  
 RT J. Biol. Chem. 270:1798-1806 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 STRAIN=CD-1; TISSUE=Kidney; Liu Z., Kanwar Y.S.;  
 RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Structural component of connective tissue microfibrils that binds calcium. Fibrillin-1-containing microfibrils provide long-term force bearing structural support.  
 CC -!- PTM: Forms intermolecular disulfide bonds either with other fibrillin-1 molecules or with other components of the microfibrils (BY similarity).  
 CC -!- SIMILARITY: Contains 47 EGF-like domains.  
 CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.

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CC EMBL; L29454; AAA56840.1; -.  
 DR EMBL; U22493; AAA64217.1; -.  
 DR PIR; A55624; A55624.  
 DR HSSP; P35555; 1APU.  
 DR MGD; MGI:95489; Fbn1.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002212; Fibrill-assoc.  
 DR Pfam; PF00008; EGF; 45.  
 DR Pfam; PF00683; TB; 9.  
 DR SMART; SM00179; EGF\_Ca; 42.  
 PROSITE; PS00017; ASX\_HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 38.  
 DR PROSITE; PS50026; EGF\_3; 45.  
 DR PROSITE; PS01187; EGF\_Ca; 43.  
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain; Repeat; Signal; Multigene family.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 2871 FIBRILLIN 1.  
 FT DOMAIN 81 112 EGF-LIKE 1.  
 FT DOMAIN 115 146 EGF-LIKE 2.



"Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase CC class-I family.

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CC DR EMBL; AF241784; AAG44472.1; -.

CC DR EMBL; AL035461; CAB55278.1; -.

CC DR EMBL; BC015333; AAH15333.1; -.

CC DR Genew; HGNC:16148; C20orf155.

CC DR InterPro; IPR000462; CDP-OH P trans.

CC DR Pfam; PF01066; CDP-OH P\_transF; 1.

CC DR PROSITE; PS00379; CDP\_ALCOHOL\_P\_TRANSF; FALSE\_NEG.

CC KW Transferase; Transmembrane.

FT TRANSMEM 179 . 199 POTENTIAL.

FT TRANSMEM 250 . 270 POTENTIAL.

FT TRANSMEM 272 . 292 POTENTIAL.

SQ SEQUENCE 301 AA; 32593 MW; 15CD406D29D3C405 CRC64;

Qy 16 GLWLALLRSVAGEQAPGTAPCSRGSWS--ADLDKCMDCAS--CRARP-----H 60

Db 9 GSWGA-LRGAA--WAPGTRPSKRACKWALLPPVPCCLGCLAAERWRLRPAALGLRLPGIGQ .65

Qy 61 SDFCLGCAAAPPAP-----FRLLW-----PILG 83

Db 66 RNHCSGAGKAAPRPAAGAGAAAEEAPGGQWGPASTPSLYENPWTIPNMLSMTIGLAPVLG 125

Qy 84 -----GALSLTFVLGLLSSGFLVWRRRERRSS 110

Db 126 YLIEEDFNIALGVFALLAGLTDLGGFIA-RNWANQRSA 163

RESULT 12

ID\_FBL4\_MOUSE STANDARD; PRT; 443 AA.

AC Q9WVJ9;

DT 16-OCT-2001 (Rel. 4.0, Created)

DT 16-OCT-2001 (Rel. 4.0, Last sequence update)

DT 15-MAR-2004 (Rel. 4.3, Last annotation update)

DE EGFR-containing fibulin-like extracellular matrix protein 2 precursor

DE (Fibulin-4) (FIBL-4) (Mutant p53 binding protein 1).

GN EFEMP2 OR FBLN4 OR MBP1.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J;

RX MEDLINE=99308589; PubMed=10380882;

RA Gallagher W.M., Argentini M., Sierra V., Bracco L., Debuissche L., Conseiller E.;

RT "MBP1: a novel mutant p53-specific protein partner with oncogenic properties.";

RT Oncogene 18:3608-3616 (1999).

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=FVB/N; TISSUE=Mammary gland;

RC MEDLINE=22388257; PubMed=1247932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Gaps 2;

Query Match 20 ALLRSVAGEQAP-----GTAPCSRGSWSADDKCMDCAS-----CRARPHSDFC 64 Best Local Similarity 28.0%; Pred. No. 16; Matches 23; Conservative 7; Mismatches 37; Indels 15; Gaps 2;

Qy 65 LGCAAAPPAPPFLLWPLIGGAL 86 Db 110 KGCYAKKFGPKGGYGGQQGGAL 191

Qy 65 LGCAAAPPAPPFLLWPLIGGAL 86 Db 110 KGCYAKKFGPKGGYGGQQGGAL 191

RESULT 15

PTTG\_HUMAN ID PTTG\_HUMAN STANDARD; PRT; 180 AA.

AC P53801; Q9NS09; DE binding factor (PBF).

AC P53801; Q9NS09; 01-OCT-1996 (Rel. 34, Created)

AC P53801; Q9NS09; 01-OCT-1996 (Rel. 34, Last sequence update)

AC P53801; Q9NS09; 15-MAR-2004 (Rel. 43, Last annotation update)

DE Pituitary tumor-transforming gene protein-binding factor (PTTG- (Pituitary tumor-transforming gene protein-binding factor) (PTTG- binding factor (PBF)).

DE PTTG1P OR C21ORF1 OR C21ORF3.

GN Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606; [1]

RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A.

RC TISSUE=Thymus; MEDLINE=98234553; PubMed=9570958; RX Yaspö M.-L., Altonen J., Horelli-Kuitunen N., Peltonen L., RA Lehrach H.; "Cloning of a novel human putative type Ia integral membrane protein mapping to 21q22.3."; RT Genomics 49:133-136 (1998). RL [2]

RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A.

RC TISSUE=Thymus; MEDLINE=20317150; PubMed=107B1616; RX Chien W., Pei L.; RA Yaspö M.-L., Altonen J., Horelli-Kuitunen N., Peltonen L., RA Lehrach H.; "A novel binding factor facilitates nuclear translocation and transcriptional activation function of the pituitary tumor-transforming gene product."; RT RT Genomics 49:133-136 (1998). RL [3]

RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A.

RC TISSUE=Colon, Lung, Muscle, and Ovary; MEDLINE=22388257; PubMed=12477932; RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA

CC -!- FUNCTION: Plays a role in cell differentiation late in myogenesis.

CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

CC -!- TISSUE SPECIFICITY: In the embryo, expression is restricted to the somatic, visceral, and pharyngeal muscles. Within the somatic musculature, MP48B is localized at the ends of muscle fibers at the point of attachment to the epidermis. There is no expression in cardiac mesoderm or in fat body.

RL Science 287:2185-2195 (2000).

CC -!- DEVELOPMENTAL STAGE: Expression is biphasic, peaking late in embryogenesis (16-24 h embryos) and during the larval to pupal transition, when the musculature is differentiating. Found in developing muscles of the visceral and somatic mesoderm subsequent to the formation of muscle precursor cells. Decreased levels are still detectable in adults.

CC -!- SIMILARITY: TO THE VERTEBRATE CYSTEINE-RICH PROTEINS.

CC -!- SIMILARITY: Contains 5 LIM zinc-binding domains.

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DR EMBL; X91245; CAA62627.1; -. DR EMBL; AF090832; AAC61591.1; -. DR EMBL; AE003672; AAF54063.1; -. DR HSSP; P32965; 1CTL.

DR FlyBase; FBgn0014863; Mlp84B.

DR InterPro; IPR001781; LIM.

DR Pfam; PF00412; LIM; 5.

DR ProdDom; PD000094; LIM; 5.

DR SMART; SM00132; LIM; 5.

DR PROSITE; PS00478; LIM\_DOMAIN\_1; 5.

DR PROSITE; PS50023; LIM\_DOMAIN\_2; 5.

KW Nuclear protein; Repeat; LIM\_domain; Metal-binding; Zinc; Myogenesis; Developmental\_protein; Differentiation.

FT DOMAIN 12 63 LIM 1.

FT DOMAIN 65 80 GLY-RICH.

FT DOMAIN 66 71 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 120 172 LIM 2.

FT DOMAIN 175 180 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 178 189 GLY-RICH.

FT DOMAIN 222 274 LIM 3.

FT DOMAIN 276 291 GLY-RICH.

FT DOMAIN 325 377 LIM 4.

Search completed: March 1, 2004, 16:43:01  
 Job time : 19 secs

---

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schein A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: May facilitate PTG1 nuclear translocation.  
 CC -!- SUBUNIT: Interacts with PTG1.  
 CC -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the  
 CC cytoplasm and in the nucleus. According to Ref.1, it is a type I  
 CC membrane protein.  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.

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 CC or send an email to license@ibb-sib.ch).

DR EMBL; Z50022; CAA90325.1;  
 DR EMBL; AF149785; AAF73770.1;  
 DR EMBL; AL163300; CAB90552.1;  
 DR EMBL; BC00415; AAH00415.1;  
 DR EMBL; BC012858; AAH12858.1;  
 DR EMBL; BC019295; AAH19295.1;  
 DR EMBL; BC020983; AAH20983.1;  
 DR EMBL; BC031097; AAH31097.1;  
 DR EMBL; BC034250; AAH34250.1;  
 DR Genew; HGNC:133524; PTG1IP.  
 DR MIM; 603784;  
 DR GO; 0005737; C:cytoplasm; IDA.  
 DR GO; GO:0016020; C:membrane; NAS.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0006606; P:protein-nucleus import; IDA.  
 DR InterPro; IPR003659; Plexin-like.  
 DR SMART; SM00423; PSI; 1.  
 KW Transmembrane; Nuclear protein.  
 FT TRANSMEM 97 117 POTENTIAL.  
 FT DOMAIN 116 121 POLY-CYS.  
 FT CONFLICT 9 19 PT PYWRLRLGG -> ARRIGGCASV (IN REF. 2).  
 FT CONFLICT 108 114 TLLGIA -> NPPPGHC (IN REF. 2).  
 SQ SEQUENCE 180 AA; 20323 MW; F1E66014D49EC1DE CRC64;

Query Match 11.3%; Score 69; DB 1; Length 180;  
 Best Local Similarity 25.8%; Pred. No. 6.9;  
 Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

QY 10 LRLVLGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPHSDFCLG--- 66  
 DB 15 LRIGGAALLLLIPVAAAQEPPGAA-CSQNTNTKTC--EECKNVSCLWCNTNKACLDYPV 71

QY 67 CAAAPPAP-----FRLW-----PILGGALSLTFLGLSGFLWRRCRER 108  
 DB 72 TSVLPASSLKLSSARRNGVCWNFEALIITMSVVG----TLLGI--AICCCCCRRKR 125

QY 109 SSPP 112  
 DB 126 SRKP 129

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:19 ; Search time 40 Seconds  
 (without alignments)  
 899.227 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608  
 Sequence: 1 MARGSLRLRLLVLGLWLA.....LSGFLVWRRCRERSSPPBX 114

. Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL\_25:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

17	75	12.3	370	4	Q96KN9
18	75	12.3	411	16	Q8CXG1
19	74.5	12.3	202	12	Q8OMP4
20	74.5	12.3	330	7	Q860W5
21	74.5	12.3	519	16	Q9A9X4
22	74	12.2	768	5	P90890
23	73.5	12.1	409	16	QB2FA3
24	73.5	12.1	730	4	Q9P2P7
25	73	12.0	227	10	O04393
26	73	12.0	243	16	QBPQD6
27	73	12.0	370	4	QBN2R7
28	73	12.0	768	13	Q98TH8
29	72.5	11.9	206	4	Q96QA0
30	72.5	11.9	242	16	Q8NNC0
31	72.5	11.9	329	4	Q9NQD2
32	72.5	11.9	346	16	Q9RSC0
33	72.5	11.9	365	4	Q9Y2B8
34	72.5	11.9	370	4	Q9BZW8
35	72.5	11.9	445	2	Q7WX79
36	72	11.8	2873	12	Q93072
37	72	11.8	721	5	Q818V6
38	71.5	11.8	210	4	Q95054
39	71.5	11.8	379	10	Q8W393
40	71.5	11.8	40	71.5	Q9IAR7
41	71	11.7	116	12	Q90631
42	71	11.7	175	16	Q9S255
43	71	11.7	308	16	Q7WR57
44	71	11.7	308	16	Q7W290
45	71	11.7	308	16	Q7VT68

#### ALIGNMENTS

RESULT 1					
ID	Q80XX9	PRELIMINARY;	PRT;	129 AA.	
AC	Q80XX9;				
DT	01-JUN-2003	(TREMBLrel. 24, Created)			
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Type 1 transmembrane protein FN14.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Mueller A.M., Giegerich G.;				
RT	"FN14, TNFRSF12a."				
RL	Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AY255102; AAP06753.1;				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
KW	Transmembrane.				
SQ	SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;				
Query Match	74.5%				
Best Local Similarity	76.1%				
Matches	86; Conservative 5; Mismatches 22; Indels 0; Gaps 0;				
QY	1 MARGSLRRRLRLVGLWLLRSGVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60				
Db	1 MAPGWPRLPQLVLGFGLVLRATAGEQAPGNAPCSSSSWSADLDKCMDCASCPARPH 60				
QY	61 SDFCLGCAAAPPAPERLLWILGGALSITFVLGLLISGFLVWRCCRERSSSPPP 113				
Db	61 SDFCLGCAAAPPAPERMLWILGGALSALVALVSGFLVWRCCRREEKFPTP 113				
RESULT 2					
Q9BZG3	Q9BZG3 PRELIMINARY;				
AC	Q9BZG3;				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	453	74.5	129	11	Q80XX9	Q80xx9 rattus norvegicus homolog
2	87	14.3	333	4	Q9BZG3	Q9bzg3 homolog
3	87	14.3	426	4	Q9BZG2	Q9bzg2 homolog
4	83.5	13.7	610	10	Q943G8	Q943g8 oryza sativa homolog
5	79.5	13.1	377	16	Q82NB0	Q82nb0 streptomyces homolog
6	79	13.0	341	6	Q90B3	Q90b3 macaca fasciata homolog
7	78.5	12.9	332	10	Q42839	Q42839 hordeum vulgare homolog
8	78.5	12.9	387	11	Q8VD70	Q8vd70 mus musculus homolog
9	77.5	12.7	219	11	Q8BM15	Q8bm15 mus musculus homolog
10	77.5	12.7	1208	11	Q80YA8	Q80ya8 mus musculus homolog
11	76.5	12.6	245	16	Q8Z5R3	Q8z5r3 salmonella homolog
12	76.5	12.6	732	16	Q81ZX4	Q81zx4 streptomyces homolog
13	75.5	12.4	222	12	Q9QE6	Q9qee6 indian citrus homolog
14	75.5	12.4	436	16	Q7U2G8	Q7u2g8 mycobacterium homolog
15	75.5	12.4	449	16	Q53668	Q53668 mycobacterium caenorhabditis homolog
16	75.5	12.4	635	5	Q182B8	Q182b8 caenorhabditis homolog



GN SAV1423.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinomycetales.  
OC Streptomycineae; Streptomyctaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
avermitilis": deducing the ability of producing secondary  
metabolites.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RL [2]  
RN RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
microorganism Streptomyces avermitilis.";  
RT Natl. Biotechnol. 21:526-531(2003).  
RL EMBL; AP005026; BAC69133.1;  
DR InterPro; IPR007016;  
DR PF04932; Wzy\_C; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 377 AA; 36860 MW; 7964E23DFEE6F29AA CRC64;

Query Match 13.1%; Score 79.5; DB 16; Length 377;  
Best Local Similarity 34.1%; Pred. No. 3.3;  
Matches 29; Conservative 10; Mismatches 33; Indels 13; Gaps 3;  
SQ SEQUENCE 377 AA; 36860 MW; 7964E23DFEE6F29AA CRC64;

Query Match 15 LGIWLALLRSVAGEQAPGTAPCSRGSSWSADL DKCMDCASCRARPHSDFCLGCAAAPPAP 74  
DB 110 LGIYLAAAPHGTAGLQ--GSSPLGPAGATAALLTLCAGAACCA-----WAARPSA 157

Query Match 75 FRLWPILGGALSLT-FVLGLLSGP 98  
DB 158 SRLALRLLAAITVTAAGAAGSLTGF 182

RESULT 6 Q9N0B3 PRELIMINARY; PRT; 341 AA.  
ID Q9N0B3;  
AC Q9N0B3;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Unnamed protein product (Gap junction protein) (Connexin).  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
NCBI\_TaxID=9541;  
RN RP SEQUENCE FROM N.A.  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
libraries."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED  
PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH  
MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL  
(CC BY SIMILARITY).  
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY  
SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.  
DR EMBL; AB046017; BAB01599.1; -.

DR GO; GO:0005922; C:connexon complex; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0015285; F:connexon channel activity; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000500; Connexin.  
DR Pfam; PF00029; connexin; 1.  
DR PRINTS; PR00206; CONNEXIN.  
DR SMART; SM00037; CNX; 1.  
DR PROSITE; PS00407; CONNEXINS\_1; 1.  
DR PROSITE; PS00408; CONNEXINS\_2; 1.  
RA Gap junction; Transmembrane.  
KW Sequence 341 AA; 36784 MW; 4A71DEA938FOFA0C CRC64;

Query Match 9 LLRLIVLGLWLLRSVAGEQAPGTAPCSRGSSWSADL DKCMDCASCRARPHSDFCLGCA 68  
Best Local Similarity 27.9%; Pred. No. 3.4;  
Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;  
SQ QY 9 LLRLIVLGLWLLRSVAGEQAPGTAPCSRGSSWSADL DKCMDCASCRARPHSDFCLGCA 68  
Db 119 LLRTLLEAAGFALNYLLFGFLAPNKFPT-----RPPTCTGVVDCY 158  
QY 69 AAPAPPAPERLWIPILGGALSLTFLVGLLUSGFLVWRCCRERESSPP 112  
Db 159 VSRPTEKSLLMLFLWAWSALSFLGLADLVLVCSLRRLMRRLRRPGPP 202

RESULT 7 Q42839 PRELIMINARY; PRT; 332 AA.  
ID Q42839;  
AC Q42839;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Chitinase (EC 3.2.1.14).  
GN CHI33.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooidae;  
OC Triticeae; Hordeum.  
NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Seed;  
RX MEDLINE=95078949; PubMed=7987416;  
RA Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,  
RA Mundy J.;  
RA RT "Identification of an enhancer/silencer sequence directing the  
aleuroone-specific expression of a barley chitinase gene.";  
RA Plant J. 6:579-589(1994).  
RL EMBL; L34211; AAA56787.1; -.  
DR PIR; T04484; T04484.  
HSSP; P23951; 2BAA.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0008843; F:endochitinase activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:005975; F:carbohydrate metabolism; IEA.  
DR GO; GO:0016998; P:cell wall catabolism; IEA.  
DR DR GO; GO:0006032; P:chitin catabolism; IEA.  
DR DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.  
DR DR InterPro; IPR001002; Chitin binding\_1.  
DR DR InterPro; IPR000726; Glyco\_Hydro\_19.  
DR DR Pfam; PF00187; Chitin\_bind\_1.  
DR DR Pfam; PF00182; Glyco\_Hydro\_19.  
DR DR PRINTS; PR00451; CHITINBINDNG.  
DR DR ProDom; PD000609; Chitin\_binding\_1.  
DR DR ProDom; PD354900; Glyco\_Hydro\_19.  
DR DR SMART; SM00270; ChBDL\_1.  
DR DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
DR DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
DR DR PROSITE; PS00026; CHITIN\_BINDING\_1.  
KW Chitin-binding; Glycosidase; Hydrolase.  
SQ SEQUENCE 332 AA; 35369 MW; 1B38554F49AC9E0F CRC64;

Query Match 12.9%; Score 78.5; DB 10; Length 332;  
 Best Local Similarity 32.0%; Pred. No. 3.7; Gaps 7;  
 Matches 33; Conservative 9; Mismatches 38; Indels 23; Gaps 7;

QY 13 LVIGLWIALRSV---AGEQAPG-TAP---CSRGSWSADLDKCMDCASCRAPHSDF 63  
 :|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DB 13 IVLSAALAMMVRAQQCGSQAGGGATCPNCLCSCRFGYCGSTSQC--GAGCQSQ---- 65  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 QY 64 CLGCCAAAPPAPERLWPILGALSITFVLGLLSSGFLVWR-RCR 105  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DB 66 CSGCGPTPPGPSP-----GGGVSSIIISRDLEEQFLLHRDRCQ 102  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 RESULT 8

QBVD70 PRELIMINARY; PRT; 387 AA.  
 ID Q8VD70; PRELIMINARY; PRT; 387 AA.  
 AC DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Similar to tumor necrosis factor receptor superfamily, member 12.  
 GN TNFRSF25 OR TNFRSF12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Salivary gland;

RA Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDJB databases.  
 RL EMBL; BC017526; AAH17526.1; -.  
 DR MGD; MGI:1934667; Trnfrsf25.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:000165; P:signal transduction; IEA.  
 DR InterPro; IPR000488; Death; 30.  
 DR InterPro; IPR006209; EGF\_1-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF000020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 SQ 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match 12.9%; Score 78.5; DB 11; Length 387;  
 Best Local Similarity 18.9%; Pred. No. 4.3;  
 Matches 35; Conservative 21; Mismatches 44; Indels 85; Gaps 7;

QY 4 GSLRRLRLWNLGLWLALLRSVAGE-----QA 30  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DD 18 GSTARVLQPLFLPLLLLILLGGQQGGMSGRCDCASESQKRYGPPCCRGCPKGHYNKA 77  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 QY 31 PGTAPC-----SRGSWSADLDKCMDC-----ASCRARP-----HS 61  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DD 78 PCAEPCGNSTCLPCPSDTFLTRDNHFKTDCTRCQVCDDEALQVTLENCSAKSDTHCGCQS 137  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 QY 62 DFLGCAAAP-----PAPFRLWPILGGALSITFVLG--LLSGFLV 100  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DB 138 GWCVDCSTEPGKSSPRFCVPGATTTPVHEAPTPFLFW--VQVLLGVAFLLGAILICAYCR 195  
 :|:|:|:|:|:|:|:|:|:|:|:  
 QY 101 WRRCR 1.05  
 :|:|:  
 DB 196 WQPCK 200  
 :|:|:  
 RESULT 9

Q8BMIS PRELIMINARY; PRT; 219 AA.  
 ID Q8BMIS

AC DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Weakly similar to neurogenic locus notch 3 protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=Forelimb;  
 MEDLINE=22354683; PubMed=12466851;  
 RC RA  
 RX RA  
 RA The FANTOM Consortium,  
 the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK031068; BAC27237.1; -.  
 PIR; PT0633; PT0633.  
 GO; GO:0005509; F:calcium ion binding; IEA.  
 InterPro; IPR000152; ASX\_hydroxyl\_S.  
 InterPro; IPR000742; EGF\_2.  
 InterPro; IPR001881; EGF\_Ca.  
 InterPro; IPR006209; EGF\_like.  
 InterPro; IPR006210; IEGF.  
 Pfam; PF00008; EGF; 2.  
 SMART; SM00181; EGF; 3.  
 SMART; SM00179; EGF\_Ca; 2.  
 PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 PROSITE; PS00022; EGF\_1; 4.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 FT NON\_TER 1  
 SQ SEQUENCE 219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;  
 Query Match 12.7%; Score 77.5; DB 11; Length 219;  
 Best Local Similarity 30.0%; Pred. No. 3.2;  
 Matches 30; Conservatve 16; Mismatches 45; Indels 9; Gaps 4;  
 DR PROSITE; PS00022; EGF\_1; 4.  
 DR 99 LAGLRCOSLDKFCBEASPLNGGTCRVAGSIFEC----TCSAGFSGQFCEVVVKTLPLPLPF 154  
 Qy 19 LALLRSVAGEQAPGTAPCSRGSFSDFCLGCAAAP-PAPP 75  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 76 RLLWPILGGALS--LTTFVLGLLSSGFLIVWRRCRERSSPPP 113  
 Qy 76 RLLWPILGGALS--LTTFVLGLLSSGFLIVWRRCRERSSPPP 113  
 Db 155 PILLEAVPAACACLLLGLLGLSGLIAARKRROSEGTYSP 194  
 RN

RESULT 10

Q8OYA8 PRELIMINARY; PRT; 1208 AA.  
 ID Q8OYA8 PRELIMINARY; PRT; 1208 AA.  
 AC DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE 5930402A21 protein (Fragment).  
 GN 5930402A21.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=C57BL/6; TISSUE=Brain;  
 MEDLINE=22388257; PubMed=12477932;  
 RC RA  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millany S.J.,  
 RA

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2] SEQUENCE FROM N.A.  
 STRAIN=C57BL/6; TISSUE=Brain;  
 Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 EMBL; BC043114; AAH43114.1; -.  
 GO; GO:0005509; F:calcium ion binding; IEA.  
 GO; GO:0005198; F:structural molecule activity; IEA.  
 InterPro; IPR000152; ASX\_hydroxy1\_S.  
 InterPro; IPR000742; EGF\_2.  
 InterPro; IPR001881; EGF\_Ca.  
 InterPro; IPR001438; EGF\_II.  
 InterPro; IPR006209; EGF\_like.  
 InterPro; IPR006210; IEGF.  
 InterPro; IPR002049; Laminin\_EGF.  
 InterPro; IPR001791; Laminin\_G.  
 Pfam; PF00008; EGF; 13.  
 PRINTS; PR00010; EGF\_BLOOD.  
 SMART; SM00011; EGFLAMININ.  
 SMART; SM00181; EGF; 15.  
 SMART; SM00179; EGF\_Ca; 13.  
 SMART; SM00282; LamG; 3.  
 PROSITE; PS00010; ASX\_HYDROXYL; 8.  
 PROSITE; PS00022; EGF\_1; 14.  
 PROSITE; PS01186; EGF\_2; 9.  
 PROSITE; PS01187; EGF\_Ca; 5.  
 PROSITE; PS50025; LAM\_G\_DOMAIN; 2.  
 NON\_TER 1 1208 AA; 126978 MW; FDFF2DF2F0B2F198 CRC64;

Query Match 12.7%; Score 77.5; DB 11; Length 1208;  
 Best Local Similarity 30.0%; Pred. No. 16;  
 Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps

b 19 LALLRSVAGEQAPGTAPCSRGSWW--SADLDKCMDCASCRARPHSDFCLGCAAAAP-PAPF 75  
 1088 LAGLRCQSLDKPCEASPCLNNGTCRVASGIFEC----TCSAGFSGQQFCEVVVKTLPLPLPF 113  
 76 RLLWPILGGALS--LTFVLGLLSGFLVWRRRERRSSPPP 113  
 1144 PILLEVAVPAACACLLLLGLLSGILAARKRQSEGTYSP 1183

RESULT 11  
 QBZ5R3 PRELIMINARY; PRT; 245 AA.  
 Q8Z5R3;  
 C 01-MAR-2002 (TreMBLrel. 20, Created)  
 T 01-MAR-2002 (TreMBLrel. 20, Last sequence update)  
 T 01-OCT-2003 (TreMBLrel. 25, Last annotation update)  
 E Flagellar biosynthetic protein Flip.  
 STY2187 OR FLIP OR T0898.  
 Salmonella typhi.  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Salmonella.  
 NCBI\_TaxID=601;  
 [1] SEQUENCE FROM N.A.  
 STRAIN=CT18;  
 MEDLINE=21534947; PubMed=11677608;  
 Parkhill J.; Dougan G.; James K.D.; Thomson N.R.; Pickard D.; Wain J.;

RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18."; Nature 413:848-852(2001).	[2]
RN	SEQUENCE FROM N.A.	
RP	STRAIN=TY2 / ATCC 700931;	
RX	MEDLINE=22531367; PubMed=12644504;	
RA	Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18.";	
RT	J. Bacteriol. 185:2330-2337(2003).	
RL	DR EMBL; AL627272; CAD05727.1; -.	
RC	DR EMBL; AE016837; AAO68576.1; -.	
RX	DR GO; GO:0019861; C:flagellum; IEA.	
RA	DR GO; GO:0016020; C:membrane; IEA.	
RT	DR GO; GO:0009306; P:protein secretion; IEA.	
RT	DR InterPro; IPR005837; FlIP.	
RT	DR InterPro; IPR005838; TypeIII_P.	
RT	DR PFam; PF00813; FlIP; 1.	
RT	DR PRINTS; PR01302; TYPE3IMPPROT.	
RT	DR PRODom; PD002586; TypeIII_P; 1.	
RT	DR TIGRFAMS; TIGR01103; FlIP; 1.	
RT	DR PROSITE; PS01060; FlIP_1; 1.	
RT	DR PROSITE; PS01061; FlIP_2; 1.	
RT	KW Flagellum; Complete proteome.	
SQ	SEQUENCE 245 AA; 26755 MW; C9B9931F0653A4D4 CRC64;	
Query Match	12.6% ; Score 76.5; DB 16; Length 245;	
Best Local Similarity	30.0% ; Pred. No. 4.5;	
Matches	33 ; Conservative 9; Mismatches 38; Indels 27; Gaps 27;	
Qy	6 IRRLLRLVGLWLALLRSVAGEQQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP---5 :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : 1 MRRLLFLSLAGLW--LFSPAAAQLPGLISQPLAGGGQSWLSVQTLVFTISLTFLPAIL 5	
Db	60 -HSDF-----CLGCAAAPPAPPFRLLWPILGGAALSLTFVL 92 :   :   :   :   :   :   :   :   :   :   : 59 LMMTSFTRIIIVFGILLRNALGTAPSAPPNQV----LLGLALFLTFIFI 100	
Qy	RESULT 12	
Db	Q81ZX4 PRELIMINARY; PRT; 732 AA. ID Q81ZX4; AC Q81ZX4; DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) DE Putative serine/threonine protein kinase. GN PKN16 OR SAV4717. OS Streptomyces avermitilis. OC Bacteria; Actinobacteria; Actinomycetales; OC Streptomycineae; Streptomyctaceae; Streptomyces. NCBI_TaxID=33903; [1] RN SEQUENCE FROM N.A. RP STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; RX MEDLINE=21477403; PubMed=11572948; RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Onoie T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism <i>Streptomyces avermitilis</i> : deducing the ability of producing secondary metabolites."; RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001). RL [2]	

SEQUENCE FROM N.A.									
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;									
RP	DR	InterPro; IPRO008891; viral_NABP.							
RC	DR	Pfam; PF05515; Viral_NABP; 1.							
RX	SQ	SEQUENCE 222 AA; 25455 MW; 636A47058DD8D01D CRC64;							
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531 (2003).									
RL	DR	EMBL; AP005040; BAC72429.1; -.							
GO;	GO:	0005524; F:ATP binding; IEA.							
GO;	GO:	0004674; F:protein serine/threonine kinase activity; IEA.							
GO;	GO:	0004713; F:protein-tirosine kinase activity; IEA.							
GO;	GO:	0006118; P:electron transport; IEA.							
GO;	GO:	0006468; P:protein amino acid phosphorylation; IEA.							
DR	InterPro; IPR002372; Bac_PQQ_repeat.								
DR	InterPro; IPR000719; Prot_kinase.								
DR	InterPro; IPR002290; Ser_thr_pk kinase.								
DR	InterPro; IPR008271; Ser_thr_pk kinase_AS.								
DR	InterPro; IPR001245; Tyr_pk kinase.								
DR	Pfam; PE00069; pk kinase; 1.								
DR	Pfam; PF01011; PQQ; 1.								
DR	ProDom; PD000001; Prot_kinase; 1.								
DR	SMART; SM00564; PQQ; 6.								
DR	SMART; SM00220; S_TK_C; 1.								
DR	SMART; SM00219; TYRKC; 1.								
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.								
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.								
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.								
KW	Kinase; Serine/threonine-protein kinase; Complete proteome.								
SQ	SEQUENCE 732 AA; 76174 MW; 41E6556B3D5EA722 CRC64;								
RA Query Match 12.6%; Score 76.5%; DB 16; Length 732; Best Local Similarity 29.2%; Pred. No. 13; Matches 35; Conservative 12; Mismatches 36; Indels 37; Gaps 7;									
Q*	2 ARGSLRRLLVGLWLALLRSVAGE--QAPGT-APCSRGS--W---SAD 45								
DB	338 ARKRLGR--RLWIPAVAVVLACVAGALVLLPGTGTGAPREQDAAPSKAQFPWDIGLSAG 395								
QY	46 LDKCMDCASCRARPHSDFC---LGCAAAPPAPERLLW-----PILGGAL 86								
Db	396 GS SKATGMAQCAVAPHRLYCTRPGVIIAAVDPADGKVLIWSRGDAKRHSDGTVRPPVLSGG 455								
RN	SEQUENCE FROM N.A.								
RP	SEQUENCE=K1;								
RC	09QEE6	PRELIMINARY; PRT; 222 AA.							
RX	09QEE6	PRELIMINARY; PRT; 222 AA.							
RA	09QEE6	PRELIMINARY; PRT; 222 AA.							
RA	01-MAY-2000 (TREMBLrel. 13, Created)								
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)								
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
DE	23kDa protein (Putative 23 kDa nucleic acid binding protein).								
OS	Indian citrus ringspot virus.								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage.								
OX	NCBI_TaxID=104664;								
RN	SEQUENCE FROM N.A.								
RP	SEQUENCE=K1;								
RC	09QEE6	PRELIMINARY; PRT; 222 AA.							
RX	09QEE6	PRELIMINARY; PRT; 222 AA.							
RA	09QEE6	PRELIMINARY; PRT; 222 AA.							
RA	01-JUN-1998 (TREMBLrel. 06, Created)								
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)								
DE	Putative membrane protein.								
GN	RV0246 OR MT0260 OR MT034.12.								
OS	Mycobacterium tuberculosis.								
OC	Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium Corynebacterineae; Mycobacteriaceae; Mycobacterium.								
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.								
RA Query Match 12.4%; Score 75.5%; DB 16; Length 436; Best Local Similarity 23.0%; Pred. No. 9.9; Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;									
QY	1 MARGSLRRLLVGLWLALLRSVAGEQA--PGTAPCSRGS--WSADDLDKMDCASCR 56								
Db	142 MPSGTARARILLTEGVGAALTAVVAATLSFVPDFQHPLSRNTHLWTAAVAMAISAAICR 201								
QY	57 ARPHSDFCCLGCAAAPPAPERLLW-----PILGG 84								
Db	202 ALPHR--IVPRVHAAPGLHVKLVYVGWTAAITNGWYRYLLVQVLFGSVVLGSSFHISRVA 259								
QY	85 -----ALSITFVFLGLLSGFLVWRRCR 105								
Db	260 AVPGDQPDEVAVVLFVCVGLLGGTIALWNVR 291								
RESULT 15									
ID	053668	PRELIMINARY; PRT; 449 AA.							
AC	053668;								
DT	01-JUN-1998 (TREMBLrel. 06, Created)								
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)								
DE	Putative membrane protein.								
GN	RV0246 OR MT0260 OR MT034.12.								
OS	Mycobacterium tuberculosis.								
OC	Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium Corynebacterineae; Mycobacteriaceae; Mycobacterium.								
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.								
RA Query Match 12.4%; Score 75.5%; DB 16; Length 436; Best Local Similarity 23.0%; Pred. No. 9.9; Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;									
QY	1 MARGSLRRLLVGLWLALLRSVAGEQA--PGTAPCSRGS--WSADDLDKMDCASCR 56								
Db	142 MPSGTARARILLTEGVGAALTAVVAATLSFVPDFQHPLSRNTHLWTAAVAMAISAAICR 201								
QY	57 ARPHSDFCCLGCAAAPPAPERLLW-----PILGG 84								
Db	202 ALPHR--IVPRVHAAPGLHVKLVYVGWTAAITNGWYRYLLVQVLFGSVVLGSSFHISRVA 259								
QY	85 -----ALSITFVFLGLLSGFLVWRRCR 105								
Db	260 AVPGDQPDEVAVVLFVCVGLLGGTIALWNVR 291								
RESULT 16									
ID	053668	PRELIMINARY; PRT; 449 AA.							
AC	053668;								
DT	01-JUN-1998 (TREMBLrel. 06, Created)								
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)								
DE	Putative membrane protein.								
GN	RV0246 OR MT0260 OR MT034.12.								
OS	Mycobacterium tuberculosis.								
OC	Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium.								
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.								
RA Query Match 12.4%; Score 75.5%; DB 16; Length 436; Best Local Similarity 23.0%; Pred. No. 9.9; Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;									
QY	1 MARGSLRRLLVGLWLALLRSVAGEQA--PGTAPCSRGS--WSADDLDKMDCASCR 56								
Db	142 MPSGTARARILLTEGVGAALTAVVAATLSFVPDFQHPLSRNTHLWTAAVAMAISAAICR 201								
QY	57 ARPHSDFCCLGCAAAPPAPERLLW-----PILGG 84								
Db	202 ALPHR--IVPRVHAAPGLHVKLVYVGWTAAITNGWYRYLLVQVLFGSVVLGSSFHISRVA 259								
QY	85 -----ALSITFVFLGLLSGFLVWRRCR 105								
Db	260 AVPGDQPDEVAVVLFVCVGLLGGTIALWNVR 291								
RESULT 17									
ID	053668	PRELIMINARY; PRT; 449 AA.							
AC	053668;								
DT	01-JUN-1998 (TREMBLrel. 06, Created)								
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)								
DE	Putative membrane protein.								

OX NCBI\_TaxID=1773;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 complete genome sequence.";  
 RL Nature 393:537-544 (1998).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Brzolaeva M., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL021929; CAA17338.1; ALT\_INIT.  
 DR EMBL; AE006934; AAK44478.1; -.  
 DR PIR; B70939; B70939.  
 DR TIGR; MT0260; -.  
 DR TuberculList; Rv0246; -.  
 DR Complete proteome.  
 SQ SEQUENCE 449 AA; 46926 MW; FCE6EF930F03D1E6 CRC64;

Query Match 12.4%; Score 75.5; DB 16; Length 449;  
 Best Local Similarity 23.0%; Pred. No. 10;  
 Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;  
 Qy 1 MARGSLRRLRLLVGLWALLRSGVAGEQA--PGTAPCSRGS--WSADLDKCMDCASCR 56  
 Db 155 MPSGTARARILLTTEVGVAALTAVVAATLSFVPDQHPLSRNTHLWTAAVAMAISAAICR 214  
 Qy 57 APHSDFCLGCAAAPPAPERFLW-----PILGG-----  
 Db 215 ALPHR--IVPRVHAAPGLHKLVYVGTAIRTNGWYRRYLVQVLFGSSVVLGSSFFHSIRVA 272  
 Qy 85 -----ALSLTFVLGLLSGFLVWRRCR 105  
 Db 273 AVPGDQPDEWTVAVVLFVCVGLLGGIALWNVR 304

Search completed: March 1, 2004, 16:43:54  
 Job time : 42 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2004, 10:32:18 ; Search time 40 Seconds  
 (without alignments)  
 452.371 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608  
 Sequence: 1 MARGSLRRRLRLYLGLWLA.....LSGFLVWRRCRERRSSPPPX 114

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Database : A\_Geneseq\_19Jun03 :\*

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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	607	99.8	114	20 AAW73409	Human secreted pro
2	571	93.9	129	20 AAW88506	Human liver clone
3	571	93.9	129	21 AAY57940	Human transmembran
4	571	93.9	129	22 AAU03498	Human TWEAK recept
5	571	93.9	129	23 ABP61512	Human NF-kB activa
6	571	93.9	129	23 AAU79827	Human type 1 trans
7	571	93.9	129	24 ABU56716	Lung cancer-associ
8	450	74.0	129	23 AAU79828	Mouse type 1 trans
9	433	71.2	309	22 AAU03500	Human TWEAK recept

Key	Misc-difference	Location/Qualifiers
XX	XX	note= "unspecified amino acid"
XX	XX	RESULT 1
XX	XX	AAW73409 standard; protein; 114 AA.
ID	AAW73409	
XX	XX	SECRETED PROTEIN
XX	XX	PATHOLOGICAL CONDITION
XX	XX	DEVELOPMENTAL ABNORMALITY
XX	XX	IMMUNE SYSTEM DISEASE
XX	XX	SCHIZOPHRENIA
DT	19-FEB-1999	(First entry)
XX	XX	HUMAN SECRETED PROTEIN ENCODED BY GENE NO. 13.
XX	XX	SECRETED PROTEIN; HUMAN; PROTEIN THERAPY; GENE THERAPY; BLOOD DISORDER; CANCER; NEUROLOGICAL DISORDER; FETAL DEFICIENCY; FOETAL DEFICIENCY; LEUKAEMIA; HEPATIC DISEASE; IMMUNE SYSTEM DISEASE; ALZHEIMER'S DISEASE; COGNITIVE DISORDER; SCHIZOPHRENIA; PROSTATE DISEASE; AUTOIMMUNE DISEASE; AIDS.
OS	OS	HOMO SAPIENS.

Key	Misc-difference	Location/Qualifiers
XX	XX	RESULT 1
XX	XX	AAW73409 standard; protein; 114 AA.
ID	AAW73409	
XX	XX	SECRETED PROTEIN
XX	XX	PATHOLOGICAL CONDITION
XX	XX	DEVELOPMENTAL ABNORMALITY
XX	XX	IMMUNE SYSTEM DISEASE
XX	XX	SCHIZOPHRENIA
DT	19-FEB-1999	(First entry)
XX	XX	HUMAN SECRETED PROTEIN ENCODED BY GENE NO. 13.
XX	XX	SECRETED PROTEIN; HUMAN; PROTEIN THERAPY; GENE THERAPY; BLOOD DISORDER; CANCER; NEUROLOGICAL DISORDER; FETAL DEFICIENCY; FOETAL DEFICIENCY; LEUKAEMIA; HEPATIC DISEASE; IMMUNE SYSTEM DISEASE; ALZHEIMER'S DISEASE; COGNITIVE DISORDER; SCHIZOPHRENIA; PROSTATE DISEASE; AUTOIMMUNE DISEASE; AIDS.
OS	OS	HOMO SAPIENS.

Key	Misc-difference	Location/Qualifiers
XX	XX	RESULT 1
XX	XX	AAW73409 standard; protein; 114 AA.
ID	AAW73409	
XX	XX	SECRETED PROTEIN
XX	XX	PATHOLOGICAL CONDITION
XX	XX	DEVELOPMENTAL ABNORMALITY
XX	XX	IMMUNE SYSTEM DISEASE
XX	XX	SCHIZOPHRENIA
DT	19-FEB-1999	(First entry)
XX	XX	HUMAN SECRETED PROTEIN ENCODED BY GENE NO. 13.
XX	XX	SECRETED PROTEIN; HUMAN; PROTEIN THERAPY; GENE THERAPY; BLOOD DISORDER; CANCER; NEUROLOGICAL DISORDER; FETAL DEFICIENCY; FOETAL DEFICIENCY; LEUKAEMIA; HEPATIC DISEASE; IMMUNE SYSTEM DISEASE; ALZHEIMER'S DISEASE; COGNITIVE DISORDER; SCHIZOPHRENIA; PROSTATE DISEASE; AUTOIMMUNE DISEASE; AIDS.
OS	OS	HOMO SAPIENS.

Key	Misc-difference	Location/Qualifiers
XX	XX	RESULT 1
XX	XX	AAW73409 standard; protein; 114 AA.
ID	AAW73409	
XX	XX	SECRETED PROTEIN
XX	XX	PATHOLOGICAL CONDITION
XX	XX	DEVELOPMENTAL ABNORMALITY
XX	XX	IMMUNE SYSTEM DISEASE
XX	XX	SCHIZOPHRENIA
DT	19-FEB-1999	(First entry)
XX	XX	HUMAN SECRETED PROTEIN ENCODED BY GENE NO. 13.
XX	XX	SECRETED PROTEIN; HUMAN; PROTEIN THERAPY; GENE THERAPY; BLOOD DISORDER; CANCER; NEUROLOGICAL DISORDER; FETAL DEFICIENCY; FOETAL DEFICIENCY; LEUKAEMIA; HEPATIC DISEASE; IMMUNE SYSTEM DISEASE; ALZHEIMER'S DISEASE; COGNITIVE DISORDER; SCHIZOPHRENIA; PROSTATE DISEASE; AUTOIMMUNE DISEASE; AIDS.
OS	OS	HOMO SAPIENS.

PR 30-MAY-1997; 97US-0048190.  
 PR 30-MAY-1997; 97US-0048356.  
 PR 30-MAY-1997; 97US-0050935.  
 PR 29-AUG-1997; 97US-0056250.  
 PR 29-AUG-1997; 97US-0056293.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Carter KC, Dillon PJ, Endress GA, Feng P, Ni J;  
 PI Rosen CA, Ruben SM, Yu G;  
 XX  
 DR WPI; 1999-070209/06.  
 DR N-PSDB; AAV08823.  
 XX  
 PT New isolated human genes - useful for diagnosis and treatment of,  
 PT e.g. cancers, neurological disorders, immune diseases, developmental  
 PT disorders or blood disorders  
 XX  
 PS Claim 11; Page 153; 188pp; English.  
 XX  
 This sequence is encoded by a cDNA of the invention, designated  
 CC Gene No. 13. This sequence represents a human secreted protein, and is  
 CC expressed in keratinocytes and to a lesser extent in endothelial  
 CC cells and placenta.  
 CC The DNA sequences of the invention and their corresponding secreted  
 CC polypeptides are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the DNA sequences.  
 CC Specific uses are described for each of the DNA sequences and the encoded  
 CC proteins, based on which tissues they are most highly expressed in, and  
 CC include developing products for the diagnosis or treatment of cancer,  
 CC tumours, neurological disorders, developmental abnormalities and foetal  
 CC deficiencies, blood disorders, leukaemias, diseases of the immune system  
 CC (including allergies or asthma), hepatic disease, Alzheimer's and  
 CC cognitive disorders, schizophrenia, prostate diseases, autoimmune  
 CC disorders and AIDS. The polypeptides are also useful for identifying  
 CC their binding partners.  
 XX  
 SQ Sequence 114 AA;

Query Match 99.8%; Score 607; DB 20; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-56;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60  
 DB 1 MARGSLRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60  
 RESULT 3  
 ID AAY57940 standard; Protein; 129 AA.

QY 61 SDFCLGCAAAPPAPFRLLWPILGALSITFVLGLLSGGFLVWRRCRRERSSPPP 113  
 DB 61 SDFCLGCAAAPPAPFRLLWPILGALSITFVLGLLSGGFLVWRRCRRERSSPPP 113  
 ID AAY57940;  
 AC  
 XX  
 DT 23-MAR-2000 (First entry)

DE Human transmembrane protein HTMPN-64.  
 XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific;  
 KW antiproliferative; neuroprotective; immune disorder;  
 KW reproductive disorder; smooth muscle disorder; neurological disorder;  
 KW gastrointestinal disorder; developmental disorder;  
 KW cell proliferative disorder.  
 XX Homo sapiens.  
 XX WO9961471-A2.  
 PN  
 PD 02-DEC-1999.  
 XX 28-MAY-1999; 99WO-US11904.  
 XX  
 PR 29-MAY-1998; 98US-0087260.  
 PR 02-JUL-1998; 98US-0091674.  
 PR 02-OCT-1998; 98US-0102954.

RESULT 2  
 RAAWB8506  
 ID AAW88506 standard; Protein; 129 AA.  
 XX AAW88506;  
 AC  
 XX  
 DT 30-MAR-1999 (First entry)  
 XX  
 DE Human liver clone HP10432-encoded membrane protein.  
 XX Transmembrane protein; HP10432; human; liver.  
 XX Homo sapiens.  
 OS  
 PN WO9855508-A2.  
 XX  
 PD 10-DEC-1998.  
 XX 03-JUN-1998; 98WO-JP02445.

PR 24-NOV-1998; 98US-0109869.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
 PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;  
 XX Au-Young J;  
 XX WPI; 2000-072605/06.  
 DR N-PSDB; AAZ56761.

PT Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders -  
 PT  
 PT  
 PT  
 PT  
 XX

PS Claim 1; Page 163; 229pp; English.

XX AAZ56698 to AAZ56776 encode AAY57955 which represent human transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN.

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 21; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERKFTTP 113

RESULT 4  
 AAU03498 ID AAU03498 standard; Protein; 129 AA.  
 XX AC AAU03498;  
 XX DT 26-SEP-2001 (First entry)  
 XX DB Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis; ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retroental fibropapilla; rubesis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis.

XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..27  
 /note= "Signal peptide"  
 FT Protein 28..129  
 /note= "Mature human TWEAKR protein"  
 FT Domain 1..78

PR /note= "Extracellular domain" 79..101  
 XX FT Domain /note= "Transmembrane domain" 102..129  
 PI /note= "Intracellular domain" WO200145730-A2.  
 XX PN 28-JUN-2001.  
 DR XX PD 19-DEC-2000; 2000WO-US34755.  
 PT XX PR 20-DEC-1999; 99US-0172878.  
 PR 10-MAY-2000; 2000US-0203347.  
 XX PA (IMMV ) IMMUNEX CORP.  
 XX PI Wiley SR;  
 XX DR WPI; 2001-417975/44.  
 DR N-PSDB; AAS03963.  
 XX PT Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK receptor -  
 PT XX PA Example 1; Fig 1; 46pp; English.  
 XX CC The sequence represents the human TWEAK receptor (TWEAKR) protein. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAK may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibropapilla, rubesis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.  
 XX SQ Sequence 129 AA;  
 XX Query Match 93.9%; Score 571; DB 22; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERKFTTP 113

XX Qy 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60  
 Db 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLXCMDCASCRARPH 60  
 Qy 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFLWLPILGALSITFVLGLLSGFLWRRCCRERKFTTP 113  
 RESULT 5  
 ABP61512 ID ABP61512 standard; Protein; 129 AA.  
 XX AC ABP61512;  
 XX DT 30-SEP-2002 (first entry)  
 XX DE Human NF- $\kappa$ B activating protein SEQ ID NO 178.  
 XX KW Human; NF- $\kappa$ B; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;

KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

XX WO200253737-A1.

XX PD 11-JUL-2002.

XX PF 25-DEC-2001; 2001WO-JP11389.

XX PR 28-DEC-2000; 2000JP-0402298.

XX PR 26-MAR-2001; 2001JP-0088912.

XX PR 24-AUG-2001; 2001JP-0254018.

XX PA (ASAHI KASEI KOGYO KK.

XX PI Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX DR WPI; 2002-583617/62.

XX DR N-PSDB; ABQ92000.

XX PT NF-approximatelyB activating gene and expressed protein, applicable in  
 PT diagnosis and screening inhibitors or promoters to control excessive  
 PT activation or inhibition for treating e.g. inflammations, autoimmune  
 PT diseases and cancer -  
 XX PS Claim 4; Page 814-815; 841pp; Japanese.

XX CC The invention relates to a purified protein (I), comprising one of 90  
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
 CC the sequences but with some amino acids deleted, substituted or added and  
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
 CC inhibitors or promoters to control excessive activation or inhibition  
 CC and for treating e.g. inflammations, autoimmune diseases, cancers  
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
 CC disorders.  
 XX SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 23; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60  
 Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60

QY 61 SDFCLGCAAAPPAPFRLWPLGGALSITFVLGLLSGFLVWRRCRRESSPPP 113  
 Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60

QY 61 SDFCLGCAAAPPAPFRLWPLGGALSITFVLGLLSGFLVWRRCRREKFTTP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPLGGALSITFVLGLLSGFLVWRRCRREKFTTP 113

RESULT 7  
 ABU56716  
 ID ABU56716 standard; Protein; 129 AA.  
 XX AC ABU56716;  
 AC ABU56716;  
 XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #309.  
 XX AC AAU79827  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human type 1 transmembrane protein Fn14.

XX KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
 KW pulmonary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
 KW tumour necrosis factor family; TNF family; TWEAK receptor;  
 KW myocardial ischaemic condition; myocardial infarction; wound healing;  
 KW burn healing; gastric ulcer; tissue transplantation;  
 KW organ transplantation; neovascularisation; vascular insufficiency;  
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
 XX OS Homo sapiens.

XX PN WO200222166-A2.

XX PD 21-MAR-2002.

XX PF 12-SEP-2001; 2001WO-US28451.

XX PR 14-SEP-2000; 2000US-232355P.

XX PA (BIOJ ) BIOGEN INC.

XX PI Browning J, Burkly L, Jakubowski A, Zheng T;  
 XX DR WPI; 2002-383103/41.

XX PT Methods of modulating angiogenesis and inhibiting tumour progression,  
 PT using TWEAK receptor agonists -  
 XX Disclosure; Fig 10A; 37pp; English.

XX CC The invention describes methods of modulating angiogenesis and inhibiting  
 CC tumour progression using TWEAK (a novel member of the tumour necrosis  
 CC factor or TNF family) receptor agonists. Conditions which can be treated  
 CC using the agonists include myocardial ischaemic conditions (e.g.  
 CC myocardial infarction), wound healing and healing of  
 CC gastric ulcers, and tissue and organ transplantation to promote  
 CC neovascularisation, particularly in subjects suffering from vascular  
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
 CC subsequently neovascularisation is useful in treatment of cancer,  
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
 CC described in the invention.

XX SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 23; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60  
 Db 1 MARGSLRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60

QY 61 SDFCLGCAAAPPAPFRLWPLGGALSITFVLGLLSGFLVWRRCRRESSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPLGGALSITFVLGLLSGFLVWRRCRREKFTTP 113

RESULT 7  
 ABU56716  
 ID ABU56716 standard; Protein; 129 AA.  
 XX AC ABU56716;  
 AC ABU56716;  
 XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #309.  
 XX AC AAU79827  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human type 1 transmembrane protein Fn14.

XX KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
 KW pulmonary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
 KW tumour necrosis factor family; TNF family; TWEAK receptor;  
 KW myocardial ischaemic condition; myocardial infarction; wound healing;  
 KW burn healing; gastric ulcer; tissue transplantation;  
 KW organ transplantation; neovascularisation; vascular insufficiency;  
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
 XX OS Homo sapiens.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PR 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.  
 PR 09-NOV-2001; 2001US-339245P.  
 PR 13-NOV-2001; 2001US-350666P.  
 PR 29-NOV-2001; 2001US-334370P.  
 PR 12-APR-2002; 2002US-372246P.  
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX PI Aziz N, Murray R;  
 XX DR WPI; 2003-093161/08.  
 XX DR N-PSDB; ABX76445.  
 XX PT Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer -  
 XX PS Claim 27; Page 429; 453pp; English.  
 XX The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, fibrosis, bronchitis, chronic obstructive pulmonary disease, emphysema, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.  
 XX Sequence 129 AA;  
 XX Query Match 93.9%; Score 571; DB 24; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 Db 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 XX Sequence 129 AA;  
 XX Query Match 93.9%; Score 571; DB 24; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 Db 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 1 MARGSLRRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLKCMDCASCRAPH 60  
 XX RESULT 9  
 AAU03500 ID AAU03500 standard; Protein; 309 AA.  
 XX AC AAU03500;  
 XX DT 26-SEP-2001 (first entry)  
 DE Human TWEAK receptor-FC (TWEAKR-FC) fusion polypeptide.  
 XX KW TWEAK receptor; TWEAK; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retinal fibroplasia;  
 KW rubosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis; human IgG1; TWEAKR-FC; fusion protein.  
 XX OS Homo sapiens.  
 XX OS Synthetic.

Key	Location/Qualifiers
FH	1. 27
Peptide	/note= "Signal peptide"
FT	28..309
FT	Protein /note= "Mature human TWEAKR-FC fusion protein. Specifically referred to in Claims 4 and 10"
FT	Domain 28..79
FT	Region 80..81 /note= "From a BgIII cloning site"
FT	Region 82..309 /note= "Fc portion"
FT	WO200145730-A2.
XX	28-JUN-2001.
XX	PD XXX 19-DEC-2000; 2000WO-US34755.
XX	PP XXX PR 20-DEC-1999; 99US-0172878.
XX	PR 10-MAY-2000; 2000US-0203347.
XX	PA (IMMV ) IMMUNEX CORP.
XX	PI XXX Wiley SR;
XX	DR WPI; 2001-417975/44.
XX	DR N-PSDB; AAS03965.
PT	Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering agonist or antagonist of TWEAK receptor -
PT	Claim 4; Page 45-46; 46pp; English.
CC	The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKR) protein extracellular domain fused to an FC portion from human IgG1. This fusion protein, TWEAKR-FC, is used in the preparation of TWEAKR agonists and antagonists. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retroental fibroplasia, rubesis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
CC	Sequence 309 AA;
CC	Query Match 71.28; Score 433; DB 22; Length 309;
CC	Best Local Similarity 74.18; Pred. No. 3.2e-37;
CC	Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;
QY	1 MARGSLRRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
DB	1 MARGSLRRLLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60
QY	61 SDFCLGCAAAPPAPERILLWPILGALSLTFLVIGLSSFLVWRRCRRERSPP 112
DB	61 SDFCLGCAAAPPAPERILL-----:-----WRSCDKTHTCPP 90

```

Query Match      45.1%;   Score 274.5;   DB 21;   Length 112;
Best Local Similarity 96.4%;   Pred. No. 4.3e-21;
Matches 54;   Conservative 1;   Mismatches 0;   Indels 1;   Gaps 1;

1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55
1 MARGSLRLLRLVGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCSTSC 56

```

cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAY26345 and AAY91450 are sequences used in the exemplification of the present invention.

RESULT 11  
 AY91604  
 D AY91604 standard; Protein; 155 AA.  
 X  
 AAY91604;  
 C  
 X  
 29-JUN-2000 (first entry)

Query Match	45.1%	Score	274.5;	DB	21;	Length	155;		
Best Local Similarity	96.4%	Pred. No.	6.1e-21;						
Matches	54;	Conservative	1;	Mismatches	0;	Indels	1;	Gaps	1;
Qy	1 MARGSLRRLLVGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55	Db	1 MARGSLRRLLVGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCTSC 56						

Query	Match	45.1%	Score	274.5	DB	21	Length	155
Best Local	Similarity	96.4%	Pred. No.	6.1e-21				
Matches	54;	Conservative	1;	Mismatches	0;	Indels	1;	
1	MARGSLRRLLRLVGLWLALLRSGVAGEQAPGTA	PCSRGSSW	SADLLDKC	MDC	C	A	-	
1	MARGSLRRLLRLVGLWLALLRSGVAGEQAPGTA	PCSRGSSW	SADLLDKC	MDC	C	A	-	

human; secreted protein; diagnosis; cytostatic; immunosuppressive antiHIV; antiinflammatory; nootropic; neuroprotective; antiallerg steopathic; antiarthritic; antibacterial; antidiabetic; antiasth antiipsoriatic; cardiant; gene therapy; cancer; neurological disor immune disease; inflammation; blood disorder; tumour; chromosome homo sapiens.

HUMA- ) HUMAN GENOME SCI INC.  
omat soulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y,  
afleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;

HUMA-) HUMAN GENOME SCI INC.  
Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
Maffleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
Oppert DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
PPI; 2000-195282/17.

new isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological

disclosure; Page 36-37; 634pp; English.

The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytosstatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiarthritic; osteopathic; antibacterial; antidiabetic; antituberculosis; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also, corresponding medical conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,

Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y; Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA; Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;

WPI: 2000-195282/17.  
N-PSDB; AAA26447.

New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -

Claim 11; Page 528; 634pp; English.

The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytoprotective; immunosuppressive; antiinflammatory; antihIV; antiarthritic; antidiabetic; antiallergic; osteopathic; antibacterial; antidiabetic; neuroprotective; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the

proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, development abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention.

Sequence 156 AA;

Query Match 45.1%; Score 274.5; DB 21; Length 156;  
Best Local Similarity 96.4%; Pred. No. 6.2e-21;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLVGLWALLRLRSVAGEQAPGTAPCSRGSWSADLKCMDCA-SC 55

Db 1 MARGSLRRLRLVGLWALLRLRSVAGEQAPGTAPCSRGSWSADLKCMDCSTSC 56

## RESULT 13

ID AAE22269 standard; Protein; 185 AA.  
XX AAE22269;

DT 25-JUL-2002 (first entry)

XX DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening; Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "Wild type Val substituted with Asn"

FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"

XX WO200224909-A2.

XX 28-MAR-2002.

XX 06-SEP-2001; 2001WO-US28006.

XX 18-SEP-2000; 2000US-233152P.

PR 21-SEP-2000; 2000US-234140P.

PR 13-FEB-2001; 2001US-268499P.

PR 14-AUG-2001; 2001US-312185P.

XX (BIOJ ) BIOGEN INC.

XX Ambrose CM, Thompson JS;

XX DR 2002-362428/39.

XX New human BAFF receptor proteins and nucleic acids, useful for

treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders -

XX PS Example 17; Page -; 164pp; English.

The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R Proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease, Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFER antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant.

Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown in Fig 2d of the specification.

XX SQ Sequence 185 AA;  
Query Match 15.5%; Score 94.5; DB 23; Length 185;  
Best Local Similarity 27.8%; Pred. No. 0.053; Mismatches 13; Indels 39; Gaps 6;  
Matches 35; Conservative 35; Matches 35; Gaps 6;  
QY 23 RSVAGEQAPGTAPCSRGSWSADLKCMDCASCRA-RPHSDFLCLGCAAAPPAPPFRLLWP-  
Db 6 RSLRGRDAPAPTPCNQAECFDLIVRHCVACGLLRTPRPKP---AGAASSPAPRTALQPQ 61  
QY 81 ---ILGA---LSLTTFVVLGL-LSGFLVWRRCRR---E 107  
Db 62 ESVGAGAGEAALPLPGLLFGAPALLGLVSLALVLVGLVSWRQRRLRGASSAEAPDGDD 121  
QY 108 RSSPPP 113  
Db 122 KDAPEP 127

RESULT 14  
ID AAE22266  
XX AAE22266 standard; Protein; 185 AA.  
AC AAE22266;  
XX DT 25-JUL-2002 (first entry)  
DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening; Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.  
XX DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.  
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening; mutant; mutein.  
XX OS Homo sapiens.

XX PT New human BAFF receptor proteins and nucleic acids, useful for  
XX PT New human BAFF receptor proteins and nucleic acids, useful for  
XX Homo sapiens.



cells disorders e.g., multiple myeloma, Waldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFRR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant.

Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.

Sequence 185 AA;

	Query	Match	Score	DB	Length
Best	Local	Similarity	15.2%	23	185;
Matches	35;	Conservative	27.8%	Pred. No.	0.086;
		Mismatches	39;	Indels	39;
				Gaps	6;
QY	23	RSVAGEQAPGTAPCSRGSWSADLDKCMDASCRA-RPHSDFCLGCAAAPPAPPRLWPLW-	80		
Db	6	RSLRGRDAPAPTPCNQTECFDLVVRHCVACGILLRTPRPKP---AGAASSPAPRTALQQ	61		
QY	81	-----ILGGA---LSLTFLVGL-LSGFLVWRRCRR-----E	107		
Db	62	ESVGAGAGEAAALPLPGILLFGAPALIGLALVLVGLSWRRRORLRGASSAEAPDGD	121		
QY	108	RSSPPP	113		
Db	122	KDAPEP	127		

Search completed: February 11, 2004, 10:38:06  
 Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: February 11, 2004, 10:36:33 ; Search time 21 Seconds  
(without alignments)  
522.059 Million cell updates/sec

Title: US-10-062-599-59  
Perfect score: 608  
Sequence: 1 MARGSLRRRLRLLVGLWLA.....LSGFLVWRRCRRERSSSPPX 114  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*

- 1: Pirl:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	78.5	12.9	332	2	T04484	probable chitinase
2	76.5	12.6	245	2	S78698	probable export pr
3	76.5	12.6	245	2	AD0753	flagellar biosynth
4	75.5	12.4	436	2	B70939	hypothetical prote
5	75.5	12.4	635	2	T20910	hypothetical prote
6	74.5	12.3	519	2	B87353	hypothetical prote
7	74	12.2	768	2	T22758	probable pyruvate
8	73.5	12.1	261	2	G69099	ribonuclease (EC 3
9	73	12.0	227	2	T04420	conserved hypothet
10	72.5	11.9	346	2	D75303	fibrillin-1 precu
11	72	11.8	2871	2	A55624	probable transcript
12	71	11.7	175	2	T36798	glypcan precursor
13	70.5	11.6	467	2	E95850	probable beta-lact
14	70	11.5	558	2	I56545	hypothetical prote
15	69.5	11.4	424	2	D75330	Fas antigen precu
16	69.5	11.4	587	2	C70893	conserved hypothet
17	69	11.3	324	2	JC2395	osmeregulated prot
18	68.5	11.3	431	1	B69092	hypothetical prote
19	68.5	11.3	484	2	E75138	probable protein k
20	68	11.2	480	2	B61213	diheme cytochrome
21	68	11.2	683	2	T00872	glycoprotein precu
22	67.5	11.1	384	1	T46966	receptor-type prot
23	67.5	11.1	1008	1	GNVUUK	bone marrow stroma
24	67.5	11.1	1013	2	I50615	oligopeptide trans
25	67	11.0	319	2	JC4390	receptor-like tyro
26	67	11.0	332	2	AH3572	receptor-like tyro
27	67	11.0	893	2	S51603	receptor-like tyro
28	67	11.0	898	2	S47489	receptor-like tyro
29	67	11.0	981	2	S51604	receptor-like tyro

## ALIGNMENTS

RESULT 1  
T04484  
probable chitinase (EC 3.2.1.14) - barley  
C;Species: *Hordeum vulgare* (barley)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
C;Accession: T04484  
R;Leah, R.; Skriver, K.; Knudsen, S.; Rund-Hansen, J.; Raikhel, N.V.; Mundy, J.  
Plant J. 6, 579-589, 1994  
A;Title: Identification of an enhancer/silencer sequence directing the aleurone-specific  
A;Reference number: Z15373; MUID:95078949; PMID:7987416  
A;Accession: T04484  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-332 <LEA>  
A;Cross-references: EMBL:134211; NID:9576566; PIDN:AAA56787.1; PID:9507961  
C;Genetics:  
A;Gene: CHI33  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; P1  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;28-69/Domain: hevein chitin-binding domain homology <HCB>  
F;85-322/Domain: plant chitinase homology <PCH>

Query Match Score 78.5; DB 2; Length 332;  
Best Local Similarity 32.0%; Pred. No. 3.5; Mismatches 9; Indels 23; Gaps 7;  
Matches 33; Conservative 33; Gaps 7;

Qy	13	LVLGLWLALLRSV---AGEQAPG-TAP---CSRGSSWSADLDKCMDCASCRARPHSDF	63
Db	13	IVLSSAALAMAVYRAQQCGSQAGGATCPNCNLCCSRFGYCGSTSDYC--GAGCQSQ-----	65
Qy	64	CLGCAAAPPAPPRLWPILGGLSFTVLGLLSGFLVWR-RCR 105	64
Db	66	CSSGGCPTPPGPSP-----GGGVSSIIISRDLFEEQLHLHRDCQ 102	66

RESULT 2  
S78698  
probable export protein flip precursor - *Salmonella typhimurium*  
C;Species: *Salmonella typhimurium*  
C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000  
C;Accession: S78698  
R;Ohnishi, K.; Fan, F.; Schoenhalz, G.J.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 179, 6092-6099, 1997  
A;Title: The Flip, Flip, and Flip proteins of *Salmonella typhimurium*: putative com  
A;Reference number: S78698; MUID:97464436; PMID:9324257  
A;Accession: S78698  
A;Molecule type: DNA  
A;Residues: 1-245 <OHN>  
A;Cross-references: EMBL:149021; NID:91066860; PID:ABB81319.1; PID:g1066863  
A;Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are 1  
C;Genetics:  
A;Gene: flip



C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
 C;Accession: B87353  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonowich, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; PMID:21173698; PMID:11259647  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-519 <STO>  
 A;Cross-references: GB:AE005673; NID:913422090; PIDN:AAB22B22.1; GSPDB:GN00148  
 C;Genetics:  
 A;Gene: CCC0837

Query	Match	Score 12.3%;	DB 2;	Length 519;
Best	Local Similarity	24.3%;	Pred. No. 12;	Gaps 4;
Matches	33;	Conservative	Mismatches 21;	Indels 31;
				Gaps 4;

QY 9 LLRLIVLGLMLALLRS-VAGEQAPGTAPCSRG-----SWSADLDKCMD 51  
 DB 250 LLILMATIGLGLFLFAAQVLGKRFADAAAATQGAETRKAAKGPGVGAFFAAGAFOATLRKELR 309  
 QY 52 CASCRARPHSDFCLGCAAAPPAPFRL-----WPIILGGALSILTFLVGLLGSFLVWRR 103  
 DB 310 LVSRDAALJSQVLLRVLYMVPIAFVMVRGAESLPAWALAGPAAVTFLAGQVAGSLIWT 369  
 QY 104 CRERS-----SPPP 113  
 DB 370 VSAEDTPDILLAISPTP 385

RESULT 7  
 T22758 hypothetical protein F55H12.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
 C;Accession: T22758  
 R;Dobson, R.  
 Submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z19610  
 A;Accession: T22758  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-768 <WIL>  
 A;Cross-references: EMBL:Z81091; PIDN:CAB03142.1; GSPDB:GN00019; CESP:F55H12.1  
 C;Genetics:  
 A;Gene: CESP:F55H12.1  
 A;Map position: 114/3; 189/1; 301/2; 426/3; 513/1; 554/3; 657/3; 687/3; 741/1  
 A;Introns: 114/3; 189/1; 301/2; 426/3; 513/1; 554/3; 657/3; 687/3; 741/1  
 C;Superfamily: gamma-amino butyric acid transporter

Query	Match	Score 12.2%;	DB 2;	Length 768;
Best	Local Similarity	40.0%;	Pred. No. 18;	Gaps 2;
Matches	20;	Conservative	Mismatches 7;	Indels 4;
				Gaps 2;

QY 52 CASCRARP--HSDFCLG---CAAAAPPAPFRLWPILGGALSILTFLVGLLGS 97  
 DB 153 CAFVFAVPAPAIHMEEFALGQYAASKSPAVFRRIMPALEGVGWMTCIVGAVIG 202

RESULT 8  
 G69099 probable pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrophicum  
 C;Species: Methanobacterium thermoautotrophicum  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-May-2000  
 C;Accession: G69099  
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Qiu, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997

QY 52 CASCRARP--HSDFCLG---CAAAAPPAPFRLWPILGGALSILTFLVGLLGS 97  
 DB 153 CAFVFAVPAPAIHMEEFALGQYAASKSPAVFRRIMPALEGVGWMTCIVGAVIG 202

RESULT 9  
 G69099 Pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrophicum  
 C;Species: Methanobacterium thermoautotrophicum  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-May-2000  
 C;Accession: G69099  
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Qiu, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997

QY 31 PGTAPCSRGSNSA-----DLDKCMDCASRA-----RPHS---DFCLGCA-APPAA 73  
 DB 191 PGSTVKNKTKGSWRTFKPVLDKDRCIDCDNCILFCPEGCINREHEIDYDYCKGGICAEKC 250

QY 74 PFRLL 78  
 DB 251 PVKAI 255

RESULT 9  
 T04420 ribonuclease (EC 3.1.-.-) - barley  
 C;Species: Hordeum vulgare (barley)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 22-Jun-1999  
 C;Accession: T04420  
 R;Rogers, J.C.; Rogers, S.W.  
 submitted to the EMBL Data Library, April 1997  
 A;Reference number: 215355  
 A;Accession: T04420  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-227 <ROG>  
 A;Cross-references: EMBL:AF000940; NID:92150001; PIDN:AAB58719.1; PID:92150002  
 A;Experimental source: cv. Igri  
 C;Genetics:  
 A;Introns: 35/3; 87/3  
 C;Superfamily: Enterobacter ribonuclease  
 C;Keywords: hydrolase

QY 12.0%; Score 73; DB 2; Length 227;  
 C;Best Local Similarity 30.0%; Pred. No. 8.8;  
 C;Matches 30; Conservative 11; Mismatches 45; Indels 14; Gaps 4;

QY 21 LLRSVAGEQAPCTTAPCSRG-SSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLW 79  
 DB 91 LLSSSLRAEWPTLACPASDGLQFWAHEWEKHGTCAQNLFHEHGKF---QTAAPPRPAPLLD 147

QY 80 PIL-----GCALSLTFLVGLL---SGFLVWRCCRERS 109  
 DB 148 ALASAGVAPDGYYTLSAVKGAIQQGTGFEPFVECNRDES 187

RESULT 10  
 D75303 conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
 C;Species: Deinococcus radiodurans  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
 C;Accession: D75303  
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vaishnav, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A;Reference number: A75250  
 A;Accession: D75303  
 A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-346 <WHI>  
A;Cross-references: GB:AE002053; PID:9646000  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR2205  
A;Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;  
Best Local Similarity 28.8%; Pred. No. 13;  
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

QY 12 LVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDCMDASC---RARPHSDD----FC 64  
Db 87 LLVTCVGLGCVL---TAGSASPWTW----MWVGALVAAGFAGVLTWHLRPAGSLFFVFA 138

QY 65 LGCAAA--PPAPFRLLWPILGGALSLSLTFVFLGILSGFLVWRRCRRERSSSPPP 113  
Db 139 VGTVGALPHPAPLPLALLAVGGAAALSVALGALGAWHSTRARPHELAAPP 189

RESULT 11  
A55624 Fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 02-Aug-2002  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, L.; Ramirez, J.; Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; PMID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: GB:L29454; NID:9575509; PID:AAA56840.1; PMID:9575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin 1; EGF homology F;1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;  
Best Local Similarity 25.3%; Pred. No. 75;  
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36 CSRGSWSADLDCMD---CASCRARPHS-----DFCLGC 67  
Db 2040 CPEGFSWSSSGRRQCDL RMSYCYAKFEGGKCSSPKSRNHSKQECCCCALKGEWWWDPCELC 2099

QY 68 AAAPPAPFRLLWPILGGAL 86  
Db 2100 PTEPDEAFRQICPFGSII 2118

RESULT 12  
T36798 probable transcription regulator soxR-like - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Accession: T36798 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21614  
A;Accession: T36798  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-175 <OLI>  
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18C  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SCI30A.18C

Query Match 11.7%; Score 71; DB 2; Length 175;

RESULT 13  
E95850 probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C;Accession: E95850  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endoc  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: E95850  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <KUR>  
A;Cross-references: GB:AI591985; PIDN:CA48469.1; PID:915139941; GSPDB:GN00167  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barloy-Hubler, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahl, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauze, hebault, P.; Vandembol, M.; vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: SMB20069  
A;Genome: plasmid  
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;  
Best Local Similarity 26.4%; Pred. No. 26;  
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLLVGLWL----ALLRSVAGEQA-PGTAPCSRGS-----SWASADLD 47  
Db 322 LATIVSGVWASGETGAVLSSAAFEALPG----YGNLYLTISLALFAFTTILGWAYAE 376

QY 48 KCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPI---LGGLALSITF 90  
Db 377 KCW-----EYLIGTASA--IPFRIWVTAFFGATLSLDF 409

RESULT 14  
I56545 glycan precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 31-Jan-2000  
C;Accession: I56545; JC1281; FC1132  
R;Litwack, E.D.; Stipp, C.S.; Kumbaras, A.; Lander, A.D.  
J;Neurosci. 14, 3713-3724, 1994  
A;Title: Neuronal expression of glypcan, a cell-surface glycosylphosphatidylinositol-an  
A;Reference number: I56545; MUID:94267529; PMID:8207484  
A;Accession: I56545  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-558 <RES>  
A;Cross-references: GB:L34067; NID:9506416; PID:AAA41251.1; PID:9506417  
R;Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.  
Biochem. Biophys. Res. Commun. 188, 395-401, 1992  
A;Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a

A;Reference number: JC12B1; MUID: 93038690; PMID:1417860  
 A;Accession: JC12B1

A;Molecule type: mRNA

A;Residues: 1-20, 'T', 22-311, 'Y', 313-361, 'A', 363-514, 'I', 516-558 <KAR>  
 A;Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425  
 A;Experimental source: brain  
 A;Accession: PC1132

A;Molecule type: protein  
 A;Residues: 24-55;424-445 <KA2>

C;Superfamily: Glypican

C;Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; heparan  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-530/Product: glypican #status predicted <MAT>  
 F;531-558/Domain: carboxyl-terminal propeptide #status predicted <CTRP>  
 F;55,486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
 F;79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;399,512/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F;530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query	Match	Score	DB	Length
Qy	Best Local Similarity	11.5%	2	558
	Matches	37.7%	Pred. No.	33
	26;	Conservative	Mismatches	6;
			Indels	19;
			Gaps	5;
Db	11 RLLVGLWLA-LLRSVAGEQAPGTTAPCSRGSWSADLDRCMDCASCR----ARPHSDFC 64			
	221 RSFVQGLGVASDVRKVA--QVPLAPECSRA----VMKLIVYCAHCRGVPGARPCCPDYC 272			
Qy	65 ----LGCAA 69			
Db	273 RNVLKGGCLA 281			

## RESULT 15

D75330 probable beta-lactamase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C;Accession: D75330  
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
 Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: D75330

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-424 <WHI>

A;Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645977

C;Genetics:

A;Gene: DR1985

A;Map position: 1

Query	Match	Score	DB	Length
Qy	Best Local Similarity	11.4%	2	424;
	Matches	29.7%	Pred. No.	30;
	30;	Conservative	Mismatches	11;
			Indels	35;
			Gaps	4;
Db	3 RGSLRRLLRLVGLWLALLRSVAGEQAPGTTAPCSRGSWSADLDRCMDCASCR-----57			
	2 RGTIRLTLAILLLG---AGINACRNREAQDTAPPAAAAQSQAAPRKAAASSPAPTATE 58			
Qy	58 ---RPHSDDFCLGCAA-----PAPFRLWPILGGALI 88			
Db	59 PAVSAPAADDGCLPAAAPAVTQAPRPPQP-----LSGRILGL 92			

Q08644	mus	musculu
P23470	homo	sapien
Q03499	hepatitis	e
O95407	homo	sapien
O95967	homo	sapien
Q01279	mus	musculu
P16283	mus	musculu
P49862	homo	sapien
O75880	homo	sapien
P17129	canis	famil
P71809	mycobacteri	
P83105	homo	sapien

protein - protein search, using sw model  
run on: February 11, 2004, 10:32:48 ; Search time 13 Seconds  
(without alignments)  
412.388 Million cell updates/sec  
little:  
US-10-0622-5999-59

scoring table: BLOSUM62   Gapop 10.0   Gapext 0.5

searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

minimum DB seq length: 0  
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

הנְּצָרָה וְהַמִּלְחָמָה

SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	571	93.9	FN14_HUMAN	129	1	Q9np84 homo sapien
2	445	73.2	FN14_MOUSE	129	1	Q9cr75 m tumor nec
3	87	14.3	T13C_HUMAN	184	1	Q96rj3 homo sapien
4	78	12.8	FBL5_RAT	448	1	Q9wvh8 rattus norv
5	77	12.7	FBL5_MOUSE	448	1	Q9wvh9 mus musculu
6	76.5	12.6	FLIP_SALTY	245	1	P54700 salmonella
7	73.5	12.1	PORD_METTH	81	1	P56815 methanobact
8	72	11.8	NPC1_HUMAN	1278	1	Q9wvj9 mus musculu
9	72	11.8	FBN1_MOUSE	2871	1	Q15118 homo sapien
10	70	11.5	FBL4_MOUSE	443	1	P35053 rattus norv
11	70	11.5	GPC1_RAT	558	1	Q61554 drosophila
12	69.5	11.4	MLP2_DROME	495	1	P53801 homo sapien
13	69	11.3	PTTG_HUMAN	180	1	Q14140 homo sapien
14	69	11.3	Y127_HUMAN	314	1	Q63199 rattus norv
15	69	11.3	TNR6_RAT	324	1	Q15499 homo sapien
16	68.5	11.3	GSCL_HUMAN	205	1	Q27719 methanobact
17	68.5	11.3	YGB4_METTH	431	1	Q9bzj7 homo sapien
18	67.5	11.1	GP62_HUMAN	368	1	P09613 wukuniemi v
19	67.5	11.1	VGLM_UK	1008	1	P54755 gallus gall
20	67.5	11.1	EPAS_CHICK	1013	1	Q63072 rattus norv
21	67	11.0	BST1_RAT	319	1	Q62424 mus musculu
22	67	11.0	HXAD_MOUSE	386	1	P54757 rattus norv
23	67	11.0	EPAS_RAT	1005	1	Q9tv36 bus scrofa
24	67	11.0	FBN1_PIG	2871	1	Q5058 cricetulus
25	66.5	10.9	FBL4_CRIGR	443	1	P42514 pseudomonas
26	66	10.9	Y6B9_PSEAE	394	1	P08563 rubella vir
27	66	10.9	POLS_RUBVM	992	1	Q9y219 homo sapien
28	66	10.9	JAG2_HUMAN	1238	1	Q61982 mus musculu
29	66	10.9	NTC3_MOUSE	2318	1	Q9r172 rattus norv
30	66	10.9	NTC3_RAT	2319	1	P33133 escherichia
31	65.5	10.8	FLIP_ECOLI	245	1	Q9um47 homo sapien
32	65.5	10.8	NTC3_HUMAN	2321	1	P22112 hom
33	65	10.7	WPA2_HUMAN	452	1	Q9r172 rattus norv

ALIGNMENTS

RESULT 1  
FN14 HUMAN  
ID FN14 HUMAN STANDARD;  
PRT; 129 AA.

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
 DE (Fibroblast growth factor-inducible immediate-early response protein  
 DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).

**Homo sapiens** (Human) .  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ISSUE=Placenta;  
MEDLINE=20216634; PubMed=10751351;  
Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,  
Testa J.R., Peifley K.A., Winkles J.A.;  
"The Fn14 immediate-early response gene is induced during liver  
regeneration and highly expressed in both human and murine  
hepatocellular carcinoma.";  
Am. J. Pathol. 156:1253-1261(2000).  
[2]  
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
Tanaka S., Sugimachi K.;  
"Human homologue of Fn14.";  
Submitted [DEC-1992] to the EMBL/GenBank/DDB/J databases.

[3] SEQUENCE FROM N.A. (ISOFORM 1).  
 TISSUE=uterus;  
 MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4]

MEDLINE=21585797; PubMed=11728344;  
 Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,  
 Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;  
 "A novel TNF receptor family member binds TWEAK and is implicated in  
 angiogenesis.";  
*Immunity* 15:837-846 (2001).  
 -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in  
 some cell types. Promotes angiogenesis and the proliferation of  
 endothelial cells. May modulate cellular adhesion to matrix  
 proteins.  
 -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
 TRAF3.  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- ALTERNATIVE PRODUCTS:  
     Event=Alternative splicing; Named isoforms=2;  
     Name=1;  
     IsoId=Q9NP84-1; Sequence=Displayed;  
     Name=2;  
     IsoId=Q9NP84-2; Sequence=VSP\_006519;  
 -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and  
 kidney. Intermediate expression in lung, skeletal muscle and  
 pancreas.  
 -!- INDUCTION: By fibroblast growth factor 1 (FGF1) and phorbol ester.  
 -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
  
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 EMBL; AF191148; AAF69108.1;  
 EMBL; AB035480; BAA94792.1;  
 EMBL; AB035481; BAB17850.1;  
 EMBL; BC002718; AAH02718.1;  
 Genew; HGNC:18152; TNFRSF12A.  
 MIM; 605914;  
 GO; GO:0006928; P:cell motility; TAS.  
 GO; GO:0007275; P:development; TAS.  
 InterPro; IPR001368; TNFR\_C6.  
 PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
 PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
 Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;  
 Alternative splicing.  
 SIGNAL                 1                 27                 POTENTIAL.  
 CHAIN                 28                 129                 TUMOR NECROSIS FACTOR RECEPTOR  
 DOMAIN                 TRANSMEM         81                 SUPERFAMILY MEMBER FN14.  
 DOMAIN                 102                 101                 EXTRACELLULAR (POTENTIAL).  
 REPEAT                 36                 129                 POTENTIAL.  
 DISULFID             36                 67                 CYTOPLASMIC (POTENTIAL).  
 DISULFID             52                 49                 TNFR-CYS (ATYPICAL).  
 VARSPLIC             33                 67                 POTENTIAL.  
 VARSPLIC             33                 67                 POTENTIAL.  
 MISSING (in isoform 2).  
 /FTID=vsp\_006519.  
 SEQUENCE             129 AA;         13911 MW;         BF3FDFB9C1E1C448 CRC64;  
  
 Query Match             93.9%;         Score 571;         DB 1;         Length 129;  
 Best Local Similarity     94.7%;         Pred. No. 7.3e-48;  
 Matches 107;         Conservative 0;         Mismatches 6;         Indels 0;         Gaps 0  
  
 1 MARGSLRLRLRLWPIAPPAPFRLWPILGALSLTFVLGLLSGFLVWRRCRRERSSSPPP 113  
 1 MARGSLRLRLWLALLRSLVAGEQAPGTAPCSRGSWSADL DKCMDCASCRARPH 60  
  
 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGLLSGFLVWRRCRRERSSSPPP 113  
 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGLLSGFLVWRRCRREREKFTTP 113



QY 108 RSSPPP 113  
 : : |  
 Db 121 KDAPEP 126

**RESULT 4**  
**FBL5\_RAT**  
 ID FBL5\_RAT STANDARD; PRT; 448 AA.  
 AC Q9WVH8; Q9R284;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest  
 DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing  
 DE protein) (EVEC).  
 GN FBLNS OR DANCE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1] RP SEQUENCE FROM N.A.  
 RX MEDLINE=99357779; PubMed=10428823;  
 RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,  
 RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  
 RA Matsunori A., Sasayama S., Chien K.-R., Honjo T.;  
 RT "DANCE, a novel secreted RGD protein expressed in developing,  
 atherosclerotic, and balloon-injured arteries.";  
 RL J. Biol. Chem. 274:22476-22483 (1999).  
 RN [2] RP SEQUENCE FROM N.A.  
 RX MEDLINE=99278197; PubMed=10347091;  
 RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;  
 RT "EVEC, a novel epidermal growth factor-like repeat-containing protein  
 upregulated in embryonic and diseased adult vasculature.";  
 RL Circ. Res. 84:1166-1176 (1999).  
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH  
 CC -!- INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR  
 CC -!- LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR  
 CC -!- DEVELOPMENT AND REMODELING.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 6 EGF-like domains.

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CC DR EMBL; AF112153; ADD41769.1; -.  
 DR EMBL; AF137350; ADD25101.1; -.  
 DR HSSP; P00736; 1APQ.  
 DR InterPro; IPR000152; ASX-hydroxyl.  
 DR InterPro; IPR001881; EGF-Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR Pfam; PF00008; EGF; 4.  
 DR SMART; SM000179; EGF CA; 4.  
 DR PROSITE; PS00010; ASX HYDROXYL; 4.  
 DR PROSITE; PS00022; EGF-1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF-2; 4.  
 DR PROSITE; PS01187; EGF-CA; 6.  
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain; Glycoprotein.

FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 448 FIBULIN-5.  
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.  
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

**RESULT 4**  
**FBL5\_MOUSE**  
 ID FBL5\_MOUSE STANDARD; PRT; 448 AA.  
 AC Q9WVH9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest  
 DE EGF-like protein) (Dance).  
 GN FBLNS OR DANCE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1] RP SEQUENCE FROM N.A.  
 RX MEDLINE=99357779; PubMed=10428823;  
 RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,  
 RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  
 RA Matsunori A., Sasayama S., Chien K.-R., Honjo T.;  
 RT "DANCE, a novel secreted RGD protein expressed in developing,  
 atherosclerotic, and balloon-injured arteries.";  
 RL J. Biol. Chem. 274:22476-22483 (1999).  
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH  
 CC -!- INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR  
 CC -!- LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR  
 CC -!- DEVELOPMENT AND REMODELING.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 6 EGF-like domains.

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DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase  
 delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).  
 DE FORD OR MTTH1740.1.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacteria; Methanobacter.  
 OX NCBI\_TaxID=187420;  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=Delta H;  
 RX MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimner G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";  
 RI J. Bacteriol. 179:7135-7155 (1997).  
 CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
 COA + CO(2) + reduced ferredoxin.  
 CC -!- SUBUNIT: HETEROCTRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
 CC GAMMA CHAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.  
 CC -!- CAUTION: THERE SEEKS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER  
 CC PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.  
 CC

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DR AE000929; AAB86210.1; ALT\_INIT.  
 DR HSSP; P00195; 1CLF.  
 DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
 DR Pfam; PF00037; Fer4; 2.  
 DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 2.  
 KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;  
 KW Complete proteome.

FT METAL	34	34	IRON-SULFUR 1 (4FE-4S) (POTENTIAL)	
FT METAL	37	37	IRON-SULFUR 1 (4FE-4S) (POTENTIAL)	
FT METAL	40	40	IRON-SULFUR 1 (4FE-4S) (POTENTIAL)	
FT METAL	44	44	IRON-SULFUR 2 (4FE-4S) (POTENTIAL)	
FT METAL	60	60	IRON-SULFUR 2 (4FE-4S) (POTENTIAL)	
FT METAL	63	63	IRON-SULFUR 2 (4FE-4S) (POTENTIAL)	
FT METAL	66	66	IRON-SULFUR 2 (4FE-4S) (POTENTIAL)	
FT METAL	70	70	IRON-SULFUR 1 (4FE-4S) (POTENTIAL)	
SQ	SEQUENCE	81 AA;	9121 MW;	219A9CCAE8A41604 CRC64;

Query Match 12.1%; Score 73.5%; DB 1; Length 81;

Best Local Similarity 29.2%; Pred. No. 1..3;  
 Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;

Qy 31 PGTAPCSRGSWSA-----DLDKCMDCASCR-----RPHS---DFCLGCA-AAPPA 73  
 Db 11 PGSTVKNKTGSWRTFKPVLDKDCKCIDCDNCILFCPEGCINREHEIDYDYCKGGICAEC 70

Qy 74 PFRLL 78  
 Db 71 PVKAI 75

- AC O15118; Q9P130;  
 AC DT 30-MAY-2000 (Rel. 39, Created)  
 AC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 AC DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Niemann-Pick C1 protein precursor.  
 GN NPC1.  
 OS Homo sapiens (Human).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1] RP SEQUENCE FROM N.A., AND VARIANTS NPC1.  
 RX MEDLINE=97362323; PubMed=9211849;  
 RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D., Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B., Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A., Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R., Blanchette-Mackie E.J., Dwyer N.K., Neufeld B.B., Chang T.-Y., Liscum L., Strauss J.F. III, Ohno K., Carmi R., Sokol J., Markie D., O'Neill R.R., van Diggelen O.P., Elleder M., Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.; RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol homeostasis";  
 RT Science 277:228-231 (1997).  
 RL RN SEQUENCE FROM N.A., AND VARIANTS.  
 RX MEDLINE=99355599; PubMed=10425213;  
 RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G., Carstea E.D.; RT "The genomic organization and polymorphism analysis of the human Niemann-Pick C1 gene.";  
 RL Biochim. Biophys. Res. Commun. 261:493-498 (1999).  
 RN [2] RP SEQUENCE FROM N.A., AND VARIANTS.  
 RX MEDLINE=21623216; PubMed=11754101;  
 RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G., Carstea E.D.; RT "The genomic organization and polymorphism analysis of the human Niemann-Pick C1 gene.";  
 RL Biochim. Biophys. Res. Commun. 261:493-498 (1999).  
 RN [3] RP SEQUENCE FROM N.A.  
 RX MEDLINE=99128318; PubMed=9927649;  
 RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J., Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.; RT "NPC1: Complete genomic sequence, mutation analysis, and characterization of haplotypes.";  
 RL Hum. Mutat. 19:30-38 (2002).  
 RN [4] RP CHARACTERIZATION.  
 RX MEDLINE=98299797; PubMed=9634529;  
 RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S., Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III; RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and lysosomal targeting of cholesterol mobilization.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810 (1999).  
 RN [5] RP VARIANT NPD TRP-992.  
 RX MEDLINE=9452586; PubMed=10521290;  
 RA Greer W.L., Riddell D.C., Gillian T.L., Girouard G.S., Sparrow S.M., Byers D.M., Dobson M.J., Neumann P.E.; RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a G3097-->T transversion in NPC1.";  
 RT Am. J. Hum. Genet. 63:52-54 (1998).  
 RL RN [6] RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007; RT THR-1061 AND VAL-1213.  
 RX MEDLINE=9452586; PubMed=10521290;  
 RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C., Neumann P.E.; RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich domain.";  
 RT Am. J. Hum. Genet. 63:52-54 (1998).  
 RL RN [7] RP VARIANT NPC1 THR-1061.  
 RX MEDLINE=99452593; PubMed=10521297;  
 RA Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A., Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.; RT "Niemann-Pick C1 disease: the I1061 substitution is a frequent mutant allele in patients of Western European descent and correlates with a classic juvenile phenotype.";

RESULT 8  
 NPC1\_HUMAN STANDARD; PRT; 1278 AA.



DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrillin 1 precursor.  
GN FBNI OR FBN-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95130561; PubMed=7829516;  
RA Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,  
RA Pereira L., Ramirez F., Bonadio J.;  
RT "Primary structure and developmental expression of Fbn-1, the mouse  
fibrillin gene.";  
RT J. Biol. Chem. 270:1798-1806 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CD-1; TISSUE=Kidney;  
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
CC -!- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER  
CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE  
CC MICROFIBRILS (BY SIMILARITY).  
CC -!- SIMILARITY: Contains 47 EGF-like domains.  
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.  
CC --- This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to license@isb-sib.ch).  
CC ---  
DR EMBL; L29454; AAA56840.1; -.  
DR EMBL; U22493; AAA64217.1; -.  
DR PIR; A55624; A55624.  
DR HSSP; P3555; IAPJ.  
DR MGD; MGI:95489; Fbn1.  
DR InterPro; IPR000152; ASX\_hydroxyl.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002212; Fibril-assoc.  
DR Pfam; PF00008; EGF; 46.  
DR Pfam; PF00683; TB; 9.  
DR SMART; SM00179; EGF\_CA; 4.2.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 43.  
DR PROSITE; PS00022; EGF\_1; 2.  
DR PROSITE; PS01186; EGF\_2; 38.  
DR PROSITE; PS01187; EGF\_CA; 4.3.  
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
KW Repeat; Signal; Multigene family.  
FT SIGNAL 1 27 PORENTIAL.  
FT CHAIN 28 2871 FIBRILLIN\_1.  
FT DOMAIN 81 112 EGF-LIKE 1.  
FT DOMAIN 115 146 EGF-LIKE 2.  
FT DOMAIN 147 178 EGF-LIKE 3.  
FT DOMAIN 246 287 EGF-LIKE 4, CALCIUM-BINDING.  
FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.  
FT DOMAIN 330 401 TGFBP\_1.  
FT DOMAIN 402 446 PRO-RICH.  
FT DOMAIN 449 489 EGF-LIKE 6.  
FT DOMAIN 490 529 EGF-LIKE 7, CALCIUM-BINDING.  
FT DOMAIN 530 571 EGF-LIKE 8, CALCIUM-BINDING.  
FT DOMAIN 572 612 EGF-LIKE 9, CALCIUM-BINDING.  
FT DOMAIN 613 653 EGF-LIKE 10, CALCIUM-BINDING.  
FT DOMAIN 656 721 TGFBP\_2.  
FT DOMAIN 723 764 EGF-LIKE 11, CALCIUM-BINDING.  
FT DOMAIN 765 806 EGF-LIKE 12, CALCIUM-BINDING.  
FT DOMAIN 807 846 EGF-LIKE 13, CALCIUM-BINDING.



QY 13 LVGLWLALLRSVAGEQAP---GTAPCSRGSWSADDKCMDCASCRARPHS----- 61  
 DB 12 LLLWAFLLLLGAASPQDPPEPDPSYTECTDGYEWDAQSQHCRDVNECLTPEACKGEMKC 71  
 QY 62 -----DECLGCAA-----PPAP 74  
 DB 72 INHYGGYLCLPRSAAVISDLHGEGPPPP 99

RESULT 11  
 GPC1\_RAT ID GPC1\_RAT STANDARD; PRT; 558 AA.  
 AC P35053;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glyican-1 precursor (HSPG M12).  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.  
 RC TISSUE=Brain;  
 RX MEDLINE=93038690; PubMed=1417860;  
 RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.; RT "Cloning of a major heparan sulfate proteoglycan from brain and identification as the rat form of glypican.";  
 RL Biochem. Biophys. Res. Commun. 188:395-401(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.  
 RC STRAIN=New England Deaconess Hospital;  
 RX MEDLINE=94267529; PubMed=8207484;  
 RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.; RT "Neuronal expression of glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan, a cell-surface protein in the adult rat nervous system.";  
 RL J. Neurosci. 14:3713-3724(1994).  
 CC -!- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE. MAY PLAY AN IMPORTANT ROLE IN THE TROPHIC AND INJURY RESPONSES OF NEURONS.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -!- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE RISE TO A MEDIUM-RELEASED SPECIES.  
 CC -!- SIMILARITY: Belongs to the glyican family.

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DR L02896; AAA86439.1; -.  
 DR L34067; AAA41251.1; -.  
 DR PIR; 156545; 156545.  
 DR InterPro; IPR001863; Glycan.  
 DR PF01153; Glycan; 1.  
 DR PS01207; GLYPICAN; 1.  
 KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor; KW Extracellular matrix.

FT SIGNAL 1 23 GLYCAN-1.  
 FT CHAIN 24 530 REMOVED IN MATURE FORM (POTENTIAL).  
 FT PROPEP 531 558 GPI-ANCHOR (POTENTIAL).  
 FT LIPID 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 116 116 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).  
 FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).  
 FT CARBOHYD 486 486 E2878A854B9A1D7F CRC64;

RESULT 11  
 GPC1\_RAT ID GPC1\_RAT STANDARD; PRT; 558 AA.  
 AC P35053;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE Glyican-1 precursor (HSPG M12).  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.  
 RC TISSUE=Brain;  
 RX MEDLINE=93038690; PubMed=1417860;  
 RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.; RT "Cloning of a major heparan sulfate proteoglycan from brain and identification as the rat form of glypican.";  
 RL Biochem. Biophys. Res. Commun. 188:395-401(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.  
 RC STRAIN=New England Deaconess Hospital;  
 RX MEDLINE=94267529; PubMed=8207484;  
 RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.; RT "Neuronal expression of glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan, a cell-surface protein in the adult rat nervous system.";  
 RL J. Neurosci. 14:3713-3724(1994).  
 CC -!- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE. MAY PLAY AN IMPORTANT ROLE IN THE TROPHIC AND INJURY RESPONSES OF NEURONS.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -!- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE RISE TO A MEDIUM-RELEASED SPECIES.  
 CC -!- SIMILARITY: Belongs to the glyican family.

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DR L02896; AAA86439.1; -.  
 DR L34067; AAA41251.1; -.  
 DR PIR; 156545; 156545.  
 DR InterPro; IPR001863; Glycan.  
 DR PF01153; Glycan; 1.  
 DR PS01207; GLYPICAN; 1.  
 KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor; KW Extracellular matrix.

FT SIGNAL 1 23 GLYCAN-1.  
 FT CHAIN 24 530 REMOVED IN MATURE FORM (POTENTIAL).  
 FT PROPEP 531 558 GPI-ANCHOR (POTENTIAL).  
 FT LIPID 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 116 116 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).  
 FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).  
 FT CARBOHYD 486 486 E2878A854B9A1D7F CRC64;

RESULT 12  
 MLP2\_DROME ID MLP2\_DROME STANDARD; PRT; 495 AA.  
 AC Q24400; Q9V162;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Muscle LIM protein MLP84B.  
 GN Drosophila melanogaster (Fruit fly).  
 OS Drosophila melanogaster  
 OC Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydrioidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A., MEDLINE=96387325; PubMed=8794860;  
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.; RT "Muscle LIM proteins associate with muscle sarcomeres and require two muscle-specific LIM proteins in Drosophila.";  
 RL J. Cell Biol. 134:1179-1195(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A., MEDLINE=96387325; PubMed=8794860;  
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.; RT "Muscle LIM proteins associate with muscle sarcomeres and require two muscle-specific LIM proteins in Drosophila.";  
 RL J. Cell Biol. 134:1179-1195(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A., STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbanya A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhadari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Dunker M., Dugan-Rocha S., Ferriera S., Fleischmann W., Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Kennison J.A., Ketchum K.A., RA

RA	Kimmel B.E., Kodaira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	QY	20 ALLRSVAGEQAP-----GTAPCSRGSWSADLDKCMDCAS-----CRARPHSDFC 64
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	Db	110 AIARAPEGEGCPRGGYVYAEQMLARGRSWHECFKCGTCKGLDSILCCEAPDKNTYC 169
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Nixon K., Nusskern D.R., Pacleb J.M.,		
RA	Nelson D.R., Nelson K.A., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	QY	65 LGCAAAPPAPERFLWPILLGGAL 86
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	Db	170 KGCYAKKPGPKGYGQGGGAL 191
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Wassarman D.A., Weinstock G.M., Weissbach J.,		
RA	Zheng X.H., Zheng F.N., Zhou X., Zhou S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of <i>Drosophila melanogaster</i> .";		
RL	Science 287:2185-2195 (2000).		
CC	-!- FUNCTION: PLAYS A ROLE IN CELL DIFFERENTIATION LATE IN MYOGENESIS.		
CC	-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.		
CC	-!- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSION IS RESTRICTED TO THE SOMATIC, VISCERAL, AND PHARYNGEAL MUSCLES. WITHIN THE SOMATIC MUSCULATURE, MLP48B IS LOCALIZED AT THE ENDS OF MUSCLE FIBERS AT THE POINT OF ATTACHMENT TO THE EPIDERMIS. THERE IS NO EXPRESSION IN CARDIAC MESODERM OR IN FAT BODY.		
CC	-!- DEVELOPMENTAL STAGE: EXPRESSION IS BIPHASIC, PEAKING LATE IN EMBRYOGENESIS (16-24 H EMBRYOS) AND DURING THE LARVAL TO PUPAL TRANSITION, WHEN THE MUSCULATURE IS DIFFERENTIATING. FOUND IN DEVELOPING MUSCLES OF THE VISCERAL AND SOMATIC MESODERM SUBSEQUENT TO THE FORMATION OF THE MUSCLE PRECURSOR CELLS. DECREASED LEVELS ARE STILL DETECTABLE IN ADULTS.		
CC	-!- SIMILARITY: TO THE VERTEBRATE CYSTEINE-RICH PROTEINS.		
CC	-!- SIMILARITY: Contains 5 LIM zinc-binding domains.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
DR	EMBL; X91245; CAA62627.1; -.		
DR	EMBL; AF090832; AAC61591.1; -.		
DR	EMBL; AE003672; AAP54063.1; -.		
DR	HSSP; P32965; ICTL.		
DR	FlyBase; FBgn0014863; Mlp84B.		
DR	InterPro; IPR001781; LIM_Pfam; PF00412; LIM; 5.		
DR	ProDom; PD000094; LIM; 5.		
DR	SMART; SM00132; LIM; 5.		
DR	PROSITE; PS00478; LIM_DOMAIN_1; 5.		
DR	PROSITE; PS50023; LIM_DOMAIN_2; 5.		
KW	Nuclear protein; Repeat; LIM_domain; Metal-binding; Zinc; Myogenesis; Developmental protein; Differentiation.		
FT	DOMAIN 12 63 LIM 1.		
FT	DOMAIN 65 80 GLY-RICH.		
FT	DOMAIN 66 71 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).		
FT	DOMAIN 120 172 LIM 2.		
FT	DOMAIN 175 180 GLY-RICH.		
FT	DOMAIN 178 189 GLY-RICH.		
FT	DOMAIN 222 274 LIM 3.		
FT	DOMAIN 276 291 GLY-RICH.		
FT	DOMAIN 325 377 LIM 4.		
FT	DOMAIN 379 390 GLY-RICH.		
FT	DOMAIN 421 473 LIM 5.		
FT	DOMAIN 475 490 GLY-RICH.		
SQ	SEQUENCE 495 AA; 53525 MW; 2E559B9178E54COE CRC64;		
Query Match	11.4%;	Score 69.5;	DB 1;
Best Local Similarity	28.0%;	Pred. No. 16;	Length 495;
Matches 23;	Conservative	7;	Mismatches 15; Gaps 2;

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., OC  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., NCBI\_TaxID=9606;  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., [1]  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: May facilitate PTRG1 nuclear translocation.  
CC -!- SUBUNIT: Interacts with PTRG1.  
CC -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the  
CC cytoplasm and in the nucleus. According to Ref.1, it is a type I  
CC membrane protein.  
CC -!- TISSUE SPECIFICITY: Ubiquitous.

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DR EMBL; Z50022; CAA90325.1; -.  
DR EMBL; AF149785; AAF73770.1; -.  
DR EMBL; AL163300; CAB90552.1; -.  
DR EMBL; BC000415; AAH00415.1; -.  
DR EMBL; BC012858; AAH12858.1; -.  
DR EMBL; BC019295; AAH19295.1; -.  
DR EMBL; BC020983; AAH20983.1; -.  
DR Genew; HGNC:13524; PTRG1IP.  
DR MIM; 603784; -.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR InterPro; IPR003659; Plexin-like.  
DR SMART; SMC00423; PSI; 1.  
KW Transmembrane; Nuclear protein.

FT TRANSMEM 97 117 POTENTIAL.  
FT DOMAIN 116 121 POLY-CYS.  
FT CONFLICT 9 19 PTPYWRLRG --> ARRTGGCASY (IN REF. 2).  
FT CONFLICT 108 114 TILLGIA --> NPPPGHC (IN REF. 2).  
SEQUENCE 180 AA; 20323 MW; FILE66014D49EC1DE CRC64; SQ

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

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AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

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AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
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AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
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Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 324 AA.  
AC Q63199; DT 15-JUL-1999 (Rel. 38, Created)  
AC AC Q63199; DT 15-JUL-1999 (Rel. 38, Last sequence update)  
AC AC Q63199; DT 15-SEP-2003 (Rel. 42, Last annotation update)  
Qy 30 APGTAPCSRGSWSADLDKCMDCASCRARPHSDFCLGC  
Db 112 SPSSHPCDLGS--TTPLEACLTTPASLLDDDDTFCTSOAMOPTAPTRKLSPPAL 162

Query Match Score 11.3%; Best Local Similarity 25.8%; Pred. No. 7; Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

RESULT 15 TNR6\_RAT ID TNR6\_RAT STANDARD; PRT; 32

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EMBL; D26112; BAA05108.1; -.  
 PIR; JC2395; JC2395.  
 HSSP; P25445; 1DDF.  
 InterPro; IPR000488; Death.  
 InterPro; IPR001368; TNFR\_C6.  
 Pfam; PF00531; death; 1.  
 SMART; SM00005; DEATH; 1.  
 SMART; SM00208; TNFR; 3.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.  
 SIGNAL 1 21 BY SIMILARITY.  
 CHAIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR  
 SUPERFAMILY MEMBER 6.  
 DOMAIN 22 171 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 172 188 POTENTIAL.  
 DOMAIN 189 324 CYTOPLASMIC (POTENTIAL).  
 REPEAT 43 79 TNFR-CYS 1.  
 REPEAT 80 123 TNFR-CYS 2.  
 REPEAT 124 163 TNFR-CYS 3.  
 DOMAIN 219 303 DEATH.  
 DISULFID 44 55 BY SIMILARITY.  
 DISULFID 56 69 BY SIMILARITY.  
 DISULFID 59 78 BY SIMILARITY.  
 DISULFID 81 97 BY SIMILARITY.  
 DISULFID 100 115 BY SIMILARITY.  
 DISULFID 103 123 BY SIMILARITY.  
 DISULFID 125 139 BY SIMILARITY.  
 DISULFID 142 154 BY SIMILARITY.  
 DISULFID 145 162 BY SIMILARITY.  
 CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SEQUENCE 324 AA; 36835 MW; D25D583C909D9D09 CRC64;  
 Query Match 11.3%; Score 69; DB 1; Length 324;  
 Best Local Similarity 18.2%; Pred. No. 12;  
 Matches 24; Conservative 18; Mismatches 34; Indels 56; Gaps 5;  
 30 APGTAPCSRGSWSAD--LDKCMDCA-----SCRAPH----- 60  
 75 APTCHPCTEGEEYTDKHYSDKRRCAFCDLEGHGLEVETNCTRQNTKCRCKENFYCNAS 134  
 61 -SDFCLGCAA-----PAPERLLWPILGALSLLTFLGLLGGFLV 100  
 101 WRRCRERSSEPP 112  
 188 YKRYRKROPGDP 199  
 135 LCDHCYHCTSCGLEFILEPCTRTSNTKCKQSSNYKLLWLPLGAILEV-----FI 187

Search completed: February 11, 2004, 10:38:33

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:35:58 ; Search time 34 Seconds  
(865.235 Million cell updates/sec  
without alignments)

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLRLVLLGLWIA.....LSGFELVWRRCRERSSSSPPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq Length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaea:\*

17 73.5 12.1 730 4 Q9P2P7 homo sapien  
18 73 12.0 227 10 Q04393 hordeum vul  
19 73 12.0 243 16 Q8PQD6 xanthomonas  
20 73 12.0 370 4 QBN2R7 homo sapien  
21 73 12.0 768 13 Q98TH8 cyprinus ca  
22 72.5 11.9 206 4 Q96OAO homo sapien  
23 72.5 11.9 242 16 Q8NNC0 corynebacte  
24 72.5 11.9 329 4 Q9NQD2 homo sapien  
25 72.5 11.9 346 16 Q9RSQ0 deinococcus  
26 72.5 11.9 365 4 Q9Y2BB homo sapien  
27 72.5 11.9 370 4 Q9BZW8 homo sapien  
28 72 11.8 368 13 Q9IAR7 gallus gall  
29 72 11.8 721 5 Q8IV6 giardia lam  
30 71.5 11.8 210 4 Q95054 homo sapien  
31 71.5 11.8 379 10 QBW393 oryza sativ  
32 71.5 11.8 2873 12 Q93072 hepatitis g  
33 71 11.7 116 12 Q90631 baboon herpes  
34 71 11.7 175 16 Q9S255 streptomyce  
35 71 11.7 473 16 Q98J10 rhizobium m  
36 71 11.7 557 11 Q9QZF2 mus musculu  
37 71 11.7 646 10 Q8RZP4 oryza sativ  
38 70.5 11.6 204 16 Q8P3W7 xanthomonas  
39 70.5 11.6 412 16 Q9FCA1  
40 70.5 11.6 467 16 Q92X93  
41 70 11.5 127 4 Q96LP0 homo sapien  
42 70 11.5 206 15 Q75637 human immun  
43 70 11.5 243 16 Q8PDE9  
44 70 11.5 293 6 Q9TT10 sus scrofa  
45 70 11.5 301 4 Q9UJA2 homo sapien

## ALIGNMENTS

RESULT 1	
ID	Description
Q9BZG3	PRELIMINARY; PRT; 333 AA.
AC	Q9BZG3;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Acid phosphatase variant 3.
GN	
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]	NCBI_TaxID=9606;
RN	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21309073; PubMed=11414767;
RA	Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT	"Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis.";
RT	Genomics 74:385-395 (2001);
RL	EMBL; AF321918; AAK09396.1; -.
DR	DR HSSP; P15309; 2HPA.
DR	InterPro; IPR000560; HisAC_Phsptse.
DR	Pfam; PF00328; acid_phosphat; 1.
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ	SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;
Query Match	14.3%; Score 87; DB 4; Length 333;
Best Local Similarity	35.3%; Pred. No. 0.45;
Matches	30; Conservate 6; Mismatches 35; Indels 14; Gaps 5;
Qy	31 PG-TAPCSRGSWSADLDKCMDASCRAPIRPHSDFCCLGC--AAAPPAPFRLLWPILGGALS 87
Db	258 PGCPAPCPFLGRFYQL-----TAPARPPAHGVSCHPYEAAIPPA---VVPLLAGAVA 307
Qy	88 LTFVIGLLSGFLVWR-RCRERRSSP 111
Db	308 VIVALSIIGLGLLAWRPGCLRALGGP 332

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	87	14.3	333	4	Q9BZG3	Q9bzg3 homo sapien
2	87	14.3	426	4	Q9BZG2	Q9bzg2 homo sapien
3	83.5	13.7	610	10	Q943G8	Q943g8 oryza sativ
4	79	13.0	341	6	Q9N0B3	Q9n0b3 macaca fasc
5	78.5	12.9	332	10	Q42839	Q42839 hordeum vul
6	78.5	12.9	387	11	Q8VDT0	Q8vd70 mus musculu
7	77.5	12.7	219	11	Q8BM15	Q8bmi5 mus musculu
8	76.5	12.6	245	16	Q8Z5R3	Q8z5r3 salmonella
9	75.5	12.4	222	12	Q9QEE6	Q9gee6 indian citr
10	75.5	12.4	449	16	Q53668	Q53668 mycobacteri
11	75.5	12.4	635	5	Q18289	O18288 caenorhabdi
12	75	12.3	370	4	Q96KN9	Q96kn9 homo sapien
13	75	12.3	411	16	Q8CXG1	Q8cxg1 oceanobacil
14	74.5	12.3	519	16	Q9A9X4	Q9a9x4 caulobacter
15	74	12.2	548	11	Q8K406	Q8k406 mus musculu
16	74	12.2	768	5	P90890	P90890 caenorhabdi

RESULT 2

ID Q9BZG2; PRELIMINARY; PRT; 426 AA.

AC Q9BZG2; DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Acid phosphatase.

GN ACPT.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

MEDLINE=21309073; PubMed=11414767;

RA Yousef G.M.; Diamandis M.; Jung K.; Diamandis E.P.;

RT "Molecular cloning of a novel human acid phosphatase gene (ACP) that is highly expressed in the testis.";

RL Genomics 74:385-395 (2001)

DR EMBL; AF321918; AAK09393.1; -.

DR HSSP; P15309; 2HFA.

DR Genew; HGNC:14376; ACPT.

DR InterPro; IPR000560; HisAC\_phosphatse.

DR Pfam; PF00328; acid phosphat; 1.

DR PROSITE; FS000616; HIS\_ACID\_PHOSPHAT\_1; 1.

DR PROSITE; FS00778; HIS\_ACID\_PHOSPHAT\_2; 1.

SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 14.3%; Score 87; DB 4; Length 426;

Best Local Similarity 35.3%; Pred. No. 0.57;

Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCSEGSSWSADLDKCMDASCRRAPHSDFCLGC--AAAPPAPFRLLWFLGGALS 87

Db 351 PGCPAPCPGLGRFYQL-----TAPARPPAAGVSVCHGPYEAIAPP-----VVFLLAGAVA 400

88 LTFVFLGLSGFLVWR-RCRRESSP 111

Db 401 VLVDSLGLGLLAWRGCLURALGGP 425

SEQUENCE FROM N.A.

Q943GB; PRELIMINARY; PRT; 610 AA.

AC Q943GB; DR PROSITE; PS00029; connexin; 1.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Putative receptor protein kinase.

GN P0046E05.12.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI\_TaxID=4530;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T.; Matsumoto T.; Yamamoto K.; "Oryza sativa nippobare(GA3)" genomic DNA, chromosome 1, PAC clone:P0046E05."

RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AP003237; BAB67905.1; -.

DR Gramene; Q943GB; -.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_Thr\_pk kinase.

DR Pfam; PF00069; pk kinase; 1.

DR ProDom; PDD00001; Prot\_kinase; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS000108; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase; Transferase.

KW

SQ SEQUENCE 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;

Query Match 13.7%; Score 83.5; DB 10; Length 610;

Best Local Similarity 24.6%; Pred. No. 1.8;

Matches 34; Conservative 12; Mismatches 35; Indels 57; Gaps 4;

QY 30 APGTAPCSRGSWSADLDKCMD----CASCRAPHSDF 63

Db 84 SPGDSSYTGGSTSATVTASTDADPNAGDAVPTSAQRKPAACRCPNRPATD- 142

QY 64 CLGCAAAPPAPPFRLLWP-----ILGGALSLTFLVGLLSSG 97

Db 143 -NVPASPPPPRISLSPPPPPSTPTQGASSGSKSSNNNTGVAVGVAVAVVVLGLAAGL 200

RESULT 4

Q9N0B3

ID Q9N0B3; PRELIMINARY; PRT; 341 AA.

AC Q9N0B3; DR 01-OCT-2000 (TREMBLrel. 15, Created)

DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Unnamed protein product (Gap junction protein) (Connexin).

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Cercopithecidae; Cercopithecinae; Macaca.

NCBI\_TaxID=9541;

RN [1]

SEQUENCE FROM N.A.

RA Osada N.; Hida M.; Kusuda J.; Tanuma R.; Iseki K.; Hirai M.; Terao K.; Suzuki Y.; Sugano S.; Hashimoto K.; RT "Isolation of full-length cDNA clones from macaque brain CDNA libraries.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL (BY SIMILARITY).

CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.

DR EMBL; AB046017; BAB01599.1; -.

DR InterPro; IPR000500; Connexin.

DR Pfam; PF000029; connexin; 1.

DR PRINTS; PR00206; CONNEXIN.

DR SMART; SM00037; CNX; 1.

DR PROSITE; PS00407; CONNEXINS\_1; 1.

DR PROSITE; PS00408; CONNEXINS\_-2; 1.

KW Gap junction; Transmembrane.

SQ SEQUENCE 341 AA; 36784 MW; 4A71DEA938FF0FA0C CRC64;

Query Match 13.0%; Score 79; DB 6; Length 341;

Best Local Similarity 27.9%; Pred. No. 3.1;

Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;

QY 9 LIRLVLIGLWLALLRLRSVAGEQAPGTAPCSRGSWSADLDKCMDASCRRAPHSDFCLGC 68

Db 119 LLRTLEAAFGALNYLFGFLAPNKFPCT-----RPPCTGVVDCY 158

QY 69 APPAPPFRLLWPILGGALSLTFLVGLLSSGFLVWRRCRRESSP 112

Db 159 VSREPTEKSLMLFLIWAWSLFLIGLADLVCSLRLMRREEGPP 202

**RESULT 5**

Q42839 PRELIMINARY; PRT; 332 AA.

ID Q42839; DR InterPro; IPR00488; Death.

AC DR InterPro; IPR006209; EGF like.

DT DR InterPro; IPR001368; TNFR\_c6.

PFam; PF00531; death; 1.

DR DR InterPro; IPRE0020; TNFR\_c6; 2.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 2.

DR PROSITE; PS50017; DBATH DOMAIN; 1.

DR PROSITE; PS01186; EGF 2; 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.

Receptor.

SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match 12.9%; Score 78.5; DB 11; Length 387;

Best Local Similarity 18.9%; Pred. No. 3.9;

Matches 35; Conservative 21; Mismatches 44; Indels 85; Gaps 7;

QA 30

RA 4 GSLRLRLRLVGLWLALLRSVAGE-----QA

Db 18 GSTARVLQPLFLPPLLLLLGGQQGGMSGRCDCASESQKRYGPFCRGCPKGHYNKA 77

QY 31 PGTAPC-----SRGSSWASADLDKCMDC-----ASCRARP-----HS 61

Db 78 PCAEPGNSTCLPCPSDTFLTRDNHFKTDCTRQVCDEEALQVTLENCSAKSDTHGCQS 137

QY 62 DFCLGCAAAP-----PAPFRLWPILGGALSLTFLVGL--LLSGFLV 100

Db 138 GWCVDCSTEPGKSSPFSCVPCGATTPVHEAPTPLFW--VQVLLGVAFILICAYCR 195

QY 101 WRRCR 105

Db 196 WQPCK 200

**RESULT 7**

Q8BM15 ID Q8BM15; PRELIMINARY; PRT; 219 AA.

AC Q8BM15;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DR 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE weakly similar to neurogenic locus notch 3 protein (Fragment).

OS Mus musculus (Mouse).

OC Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Forelimb;

RC MEDLINE=22354683; PubMed=12466851;

RX The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RT Nature 420:563-573 (2002).

DR EMBL; AK031068; BAC27237.1; -.

FT NON\_TER 1 1

SEQQUENCE 219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;

Query Match 12.7%; Score 77.5; DB 11; Length 219;

Best Local Similarity 30.0%; Pred. No. 2.9;

Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

QY 19 LALLRSVAGEQAPGTAPCSRGSSW--SADLDKCMDCASCRAPHSDFCLGCAAAP-PAPPF 75

Db 99 LAGURCQSLDKPCEASPLCLNGGTCRVAGIFEC----TCSAGFSGQFCEVVVKTLPLIPF 154

QY 76 RLLWPILGGALS--LTFVLGLLSGGFLWNRRCRRRSSPPP 113

Db 155 PLLEVAVPAACACLLLMLGLSGILAAKRRQSEGTYSP 194

**RESULT 6**

Q8VD70 ID Q8VD70; PRELIMINARY; PRT; 387 AA.

AC Q8VD70; DR InterPro; IPR002002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Similar to tumor necrosis factor receptor superfamily, member 12.

GN TNFRSF25 OR TNFRSF12.

OS Mus musculus (Mouse).

OC Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN SEQUENCE FROM N.A.

RC Salivary gland;

RA Strausberg R.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC017526; AAB17526.1; -.

DR MGDS; MGI;1934667; Tnfrsf25.



RESULT 11  
 118288 PRELIMINARY; PRT; 635 AA.  
 O 018288  
 C 018288;  
 C 01-JAN-1998 (TREMBIrel. 05, Created)  
 C 01-MAY-1999 (TREMBIrel. 10, Last sequence update)  
 C 01-MAR-2003 (TREMBIrel. 23, Last annotation update)  
 T ZK1010.9 protein.  
 E ZK1010.9.  
 N Caenorhabditis elegans.  
 S Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 S Rhabditidae; Peloderaiae; Caenorhabditis.  
 NCBI\_TaxID=6239;  
 [1]  
 SEQUENCE FROM N.A.

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; Z81503; CAB04115.1; -.  
EMBL; Z82083; CAB04115.1; JOINED.  
EMBL; Z82083; CAB04975.1; -.  
EMBL; Z81503; CAB04975.1; JOINED.  
WormPep; ZK1010.9; CE23490.  
InterPro; IPR000175; Na/ntran\_symport.

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PRINTS; PR00176; NAMEUSMPORT.
PRODOM; PD000448; Na/ntrn_symport; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMPP_3; 1.
Hypothetical protein.
SEQUENCE 635 AA; 71267 MW; 2841834039D8F14A CRC64;

```

87 SLTFVLGLLSSG 97  
149 WMTCLVGAIIG 159

DR EMBL; AFU04338; BAC13682.1; - .  
KW Complete proteome.  
SQ SEQUENCE 411 AA;  
45188 MW;  
589B48F6EC39275A CRC64;  
RESULT 12

[1] SEQUENCE FROM N.A.  
Eibergen J.; Soehl G.; Willecke K.;

DEPOSIT 14

Q9A9X4 PRELIMINARY; PRT; 519 AA.  
 Q9A9X4; PRT; 519 AA.  
 ID 01-JUN-2001 (TREMBrel. 17, Created)  
 AC 01-JUN-2001 (TREMBrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)  
 DE HYPothetical protein CC0837.  
 CC0837.  
 CN Caulobacter crescentus.  
 DS Bacteria; Proteobacteria; Alpha proteobacteria; Caulobacterales;  
 DC Caulobacteraceae; Caulobacter.  
 DC NCBI\_TaxID=155892;  
 DX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
 Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 "Complete genome sequence of Caulobacter crescentus.";  
 Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 EMBL; AE005760; AAC22822.1; -.  
 TIGR; CC0837; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;  
 Query Match 12.3%; Score 74.5; DB 16; Length 519;  
 Best Local Similarity 24.3%; Pred. No. 13;  
 Matches 33; Conservative 21; Mismatches 51; Indels 31; Gaps 4;  
 QY 9 LIRLLVGLWLLRLRS-VAGEQAPGTAPCSRGS--SWSADLDKCMD 51  
 Ddb 250 LLIILMAIGLGLFLFAAQVLGKRFDAAAATQGAETRKAAKGPVGAFAAAGAFQATLRKEELR 309  
 QY 52 CASCRARPHSDDFCLGGCAAAPPAPFRLL--WPILGGALSITFVLGLLSGELVWRR 103  
 Ddb 310 LVSRDAALLSQVLLRVLYMVPIAFMVRGAESLPAWALLAATFLAGQVAGSLIWIT 369  
 QY 104 CRRERS-----SPPP 113  
 Ddb 370 VSAEDTPDLLAISPTP 385

RESULT 15  
 Q8K406 PRELIMINARY; PRT; 548 AA.  
 Q8K406; PRT; 548 AA.  
 ID 01-OCT-2002 (TREMBrel. 22, Created)  
 AC 01-OCT-2002 (TREMBrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)  
 DE Leubrin/leucine-rich glioma inactivated 1-like protein (weakly similar to leucine-rich glioma-inactivated 1 protein).  
 DE LGI3.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=CS7BL/6J; TISSUE=Hippocampus;  
 RC MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RA

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:37:18 ; Search time 21 Seconds

(without alignments)  
 229.688 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608

Sequence: 1 MARGSLRRRLRLLVGLWLA.....LSGFLVWRRCRRERSSSPPFX 114

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:/\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:/\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:/\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:/\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:/\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	4 US-09-690-454-59	Sequence 59, Appl
2	274.5	45.1	112	4 US-09-489-847-139	Sequence 139, App
3	274.5	45.1	155	4 US-09-489-847-284	Sequence 284, App
4	274.5	45.1	156	4 US-09-489-847-228	Sequence 228, App
5	96.5	15.9	248	4 US-09-252-991A-29249	Sequence 29249, A
6	88.5	14.6	400	4 US-09-252-991A-26145	Sequence 26145, A
7	87.5	14.4	631	4 US-09-252-991A-20063	Sequence 20063, A
8	83.5	13.7	152	4 US-09-252-991A-31619	Sequence 31619, A
9	80.5	13.2	249	4 US-09-252-991A-29850	Sequence 29850, A
10	76.5	12.6	250	4 US-09-322-409-31	Sequence 31, Appl
11	76.5	12.6	276	4 US-09-451-527-31	Sequence 31, Appl
12	76.5	12.6	276	4 US-09-451-527-26	Sequence 26, Appl
13	76.5	12.6	276	4 US-09-451-527-26	Sequence 26, Appl
14	75	12.3	334	4 US-09-252-991A-18795	Sequence 18795, A
15	74.5	12.3	305	4 US-09-252-991A-21147	Sequence 21147, A
16	73.5	12.1	187	4 US-09-199-637A-287	Sequence 287, App
17	73.5	12.1	187	4 US-09-252-991A-21454	Sequence 21454, A
18	72	11.8	1278	4 US-09-462-136-2	Sequence 2, Appl
19	72	11.8	3724	2 US-08-804-227C-10	Sequence 4, Appl
20	72	11.8	3724	2 US-09-252-991A-22078	Sequence 22078, A
21	71.5	11.8	478	4 US-09-252-991A-18195	Sequence 18195, A
22	70.5	11.6	402	4 US-09-252-991A-231	Sequence 231, App
23	70	11.5	720	4 US-09-996-243-231	Sequence 25290, A
24	69.5	11.4	176	4 US-09-252-991A-24730	Sequence 24730, A
25	69	11.3	152	4 US-09-252-991A-20688	Sequence 20688, A
26	69	11.3	153	4 US-09-220-528-104	Sequence 104, App
27	69	11.3	215	3 US-09-220-528-104	

#### ALIGNMENTS

RESULT 1 US-09-690-454-59					
; Sequence 59, Application US/09690454					
; Patent No. 653147					
; GENERAL INFORMATION:					
; APPLICANT: Steven M. Ruben, et al.					
; TITLE OF INVENTION: 32 Human Secreted Proteins					
; FILE REFERENCE: PZ006P1					
; CURRENT APPLICATION NUMBER: US/09/690,454					
; CURRENT FILING DATE: 2000-10-18					
; PRIOR APPLICATION NUMBER: 09/189, 144					
; PRIOR FILING DATE: 1998-11-10					
; PRIOR APPLICATION NUMBER: 60/044, 039					
; PRIOR FILING DATE: May 30, 1997					
; PRIOR APPLICATION NUMBER: 60/048, 093					
; PRIOR FILING DATE: May 30, 1997					
; PRIOR APPLICATION NUMBER: 60/048, 190					
; PRIOR FILING DATE: May 30, 1997					
; PRIOR APPLICATION NUMBER: 60/048, 101					
; PRIOR FILING DATE: May 30, 1997					
; PRIOR APPLICATION NUMBER: 60/048, 356					
; PRIOR FILING DATE: May 30, 1997					
; PRIOR APPLICATION NUMBER: 60/056, 250					
; PRIOR FILING DATE: August 29, 1997					
; PRIOR APPLICATION NUMBER: 60/056, 296					
; PRIOR FILING DATE: August 29, 1997					
; PRIOR APPLICATION NUMBER: 60/056, 293					
; PRIOR FILING DATE: August 29, 1997					
; NUMBER OF SEQ ID NOS: 229					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO: 59					
; LENGTH: 114					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; FEATURE:					
; NAME/KEY: SITE					
; LOCATION: (114)					
; OTHER INFORMATION: Xaa equals stop translation					
; US-09-690-454-59					
; Query Match 99.8%; Score 607; DB 4; Length 114;					
; Best Local Similarity 100.0%; Pred. No. 4.5e-59;					
; Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
; Qy 1 MARGSLRRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRAPH 60					
; Db 1 MARGSLRRRLRLLVGLWALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRAPH 60					

QY 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLVWRRCRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSITFVLGLLSGFLVWRRCRERSSPPP 113

RESULT 2  
 US-09-489-847-139  
 ; Sequence 139, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-07-30  
 ; EARLIER APPLICATION NUMBER: 60/095, 486  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/095, 455  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 139  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-489-847-139

Query Match 45.1%; Score 274.5; DB 4; Length 112;  
 Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55

RESULT 3  
 US-09-489-847-284  
 ; Sequence 284, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 284  
 ; LENGTH: 155  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-489-847-284

Query Match 45.1%; Score 274.5; DB 4; Length 155;  
 Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55

RESULT 4  
 US-09-489-847-228  
 ; Sequence 228, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secreted Proteins  
 ; FILE REFERENCE: PZ031P1  
 ; CURRENT APPLICATION NUMBER: US/09/489, 847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29  
 ; EARLIER APPLICATION NUMBER: 60/094, 657  
 ; EARLIER FILING DATE: 1998-07-30  
 ; EARLIER APPLICATION NUMBER: 60/095, 486  
 ; EARLIER FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/096, 319  
 ; EARLIER FILING DATE: 1998-08-12  
 ; EARLIER APPLICATION NUMBER: 60/095, 454  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/095, 455  
 ; EARLIER FILING DATE: 1998-08-06  
 ; NUMBER OF SEQ ID NOS: 376  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 228  
 ; LENGTH: 156  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (156)  
 ; OTHER INFORMATION: Xaa equals stop translation  
 ; US-09-489-847-228

Query Match 45.1%; Score 274.5; DB 4; Length 156;  
 Best Local Similarity 96.4%; Pred. No. 1.3e-22;  
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55

RESULT 5  
 US-09-252-991A-29249  
 ; Sequence 29249, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074, 788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094, 190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 29249  
 ; LENGTH: 248  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-489-847-284

US-09-252-991A-29249

Query Match 15.9%; Score 96.5; DB 4; Length 248;  
Best Local Similarity 30.0%; Pred. No. 0.0062;  
Matches 27; Conservative 9; Mismatches 23; Indels 31; Gaps 4;

Qy 18 WLLLRSVAGE-----QAPGTAPCSRGS-----SWSADLDKCM 50  
Db 38 WCSSTRSGGAACRRCRASSTAPCSRASPATAAPRTTRTGSNCWAGAAAPTCSATTSCR 97

RESULT 6  
Sequence 26145, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
PRIORITY FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 26145  
LENGTH: 400  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26145

Query Match 14.6%; Score 88.5; DB 4; Length 400;  
Best Local Similarity 38.3%; Pred. No. 0.08;  
Matches 23; Conservative 4; Mismatches 30; Indels 3; Gaps 2;

Qy 18 WLLLRSVAGEQAPGTAPCS--RGSSWSADLDKCMDCASCRAPHSDFCLGCA-AAPPAP 74  
Db 45 WSTAWRFPPTAAAGWPRCAWMASNWTATLSPTSTASCRPMPHRSCACCAKSRRPAP 104

RESULT 7  
US-09-252-991A-20063  
Sequence 20063, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
PRIORITY FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20063  
LENGTH: 631  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20063

Query Match 14.4%; Score 87.5; DB 4; Length 631;  
Best Local Similarity 32.6%; Pred. No. 0.17;  
Matches 30; Conservative 6; Mismatches 43; Indels 13; Gaps 4;

Qy 23 RSVAGEQAPGTAPCSRGS-SWS-ADLDKCM--DCASCRAPHSDFCLGCAAAPPAPRLL 78  
Db 23 RSVAGEQAPGTAPCSRGS-SWS-ADLDKCM--DCASCRAPHSDFCLGCAAAPPAPRLL 78

RESULT 8  
US-09-252-991A-31619  
Sequence 31619, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
PRIORITY FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 31619  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31619

Query Match 13.7%; Score 83.5; DB 4; Length 152;  
Best Local Similarity 29.7%; Pred. No. 0.092;  
Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;

Qy 23 RSVAGEQAPGTAPCSRGSWSADLDKCMDC----ASC--RARPHSDFCLGCAAPPAP 74  
Db 63 RTTSNARPTPARCSRHAPGWLGSTRACTCGAAACGASCASTARPTT---TAANPPSS 117

Query Match 13.7%; Score 83.5; DB 4; Length 152;  
Best Local Similarity 29.7%; Pred. No. 0.092;  
Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;

Qy 75 FRLLWPILGGALSITFVLGLLSGFLVWRRCCRRE---RSSPP 112  
Db 118 APATWSASGGRCAGN----WRRCNRAANGWQRQSPP 147

RESULT 9  
US-09-252-991A-29850  
Sequence 29850, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
PRIORITY FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 29850  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29850

Query Match 13.2%; Score 80.5; DB 4; Length 249;  
Best Local Similarity 30.5%; Pred. No. 0.35;  
Matches 40; Conservative 8; Mismatches 32; Indels 51; Gaps 8;

Qy 10 LRLVVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC-----RA 57  
Db 104 LRAVRLAFCRILRAVAGARLVAAP--RGAGLAAPAQS--PAACSCANTSRSSTFAPLRI 159

QY 58 RP-----HSDFCLGCA-AAPPAPERLW-----PILGGALSLTFVGLLSSGFLV 100 ; ORGANISM: Canis familiaris  
Db 160 RPTESPRRSRSCQAASAATPAPSATLWVLVKHRRMAPI---SLSLT---- 205

Query Match 12.6%; Score 76.5; DB 4; Length 250;  
Best Local Similarity 27.5%; Pred. No. 0.95;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLLVLGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
Db 49 RLVLAQRMWVRQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQQLAAALKPWTIRRNFG 108

RESULT 10  
US-09-322-409-31  
; Sequence 31, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; US-09-322-409-31

Query Match 12.6%; Score 76.5; DB 4; Length 250;  
Best Local Similarity 27.5%; Pred. No. 0.95;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLLVLGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
Db 49 RLVLAQRMWVRQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQQLAAALKPWTIRRNFG 108

QY 45 DLD-KCMDCASCRARPHSDFCLGCAA-APPAPERLWPILGALSLTFVGLLSSGFLVW 101  
Db 109 CLELQCQPDSSTLVPPRSPGALEATALPAPQAP-RLLLLL--LPVALLLMSTAACLHW 164

QY 102 RRCRERSSP 112  
Db 165 RRRRRRSPP 175

RESULT 12  
US-09-322-409-26  
; Sequence 26, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; US-09-322-409-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;  
Best Local Similarity 27.5%; Pred. No. 1.1;  
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLLVLGLWLALLRSVAG-----EQAPGTAPCSRGSWSA 44  
Db 75 RLVLAQRMWVRQAVAGSQMQLLEAVNTEIHFTFCAFQDTSQQLAAALKPWTIRRNFG 134

QY 45 DLD-KCMDCASCRARPHSDFCLGCAA-APPAPERLWPILGALSLTFVGLLSSGFLVW 101  
Db 135 CLELQCQPDSSTLVPPRSPGALEATALPAPQAP-RLLLLL--LPVALLLMSTAACLHW 190

QY 102 RRCRERSSP 112  
Db 191 RRRRRRSPP 201

RESULT 13  
US-09-451-527-26  
; Sequence 26, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 250  
; TYPE: PRT



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:39:29 ; Search time 34 Seconds  
 (without alignments)  
 702.046 Million cell updates/sec

Title: US-10-062-599-59  
 Perfect score: 608  
 Sequence: 1 MARGSLRLLRLVIGLWIA.....LSGFLIVRRRCRERSSPPPX 114

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/us07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cmn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/us08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/us08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/us09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/us09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/us09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/us09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/us10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/us10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/us10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/us60\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/us60\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/us60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	607	99.8	114	12	US-10-062-599-59
2	607	99.8	114	15	US-10-062-831-59
3	571	93.9	129	9	US-09-742-454A-4
4	571	93.9	129	10	US-09-883-777-4
5	571	93.9	129	12	US-10-024-298A-178
6	571	93.9	129	12	US-10-042-211A-178
7	571	93.9	129	12	US-10-331-496A-37
8	571	93.9	129	12	US-10-295-027-444
9	571	93.9	129	12	US-10-295-027-1305
10	450	74.0	129	9	US-09-742-454A-5
11	450	74.0	129	10	US-09-883-777-5
12	433	71.2	309	9	US-09-742-454A-7
13	433	71.2	309	10	US-09-883-777-7
14	379.5	62.4	300	10	US-09-883-777-9
15	97.5	16.0	171	15	US-10-251-947-4

## ALIGNMENTS

RESULT 1  
 US-10-062-599-59  
 ; Sequence 59, Application US/10062599  
 ; Publication No. US20030195346A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Steven M. Ruben, et al.  
 ; TITLE OF INVENTION: 32 Human Secreted Proteins  
 ; FILE REFERENCE: PZ006P1  
 ; CURRENT APPLICATION NUMBER: US/10/062,599  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 09/690,454  
 ; PRIOR FILING DATE: 2000-10-18  
 ; PRIOR APPLICATION NUMBER: 09/189,144  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048,190  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/050,935  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048,101  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048,356  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056,250  
 ; PRIOR FILING DATE: August 29, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056,296  
 ; PRIOR FILING DATE: August 29, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056,293  
 ; PRIOR FILING DATE: August 29, 1997  
 ; NUMBER OF SEQ ID NOS: 229  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 59  
 ; LENGTH: 114  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

FEATURE: SITE  
 NAME/KEY: SITE  
 LOCATION: (114)  
 OTHER INFORMATION: Xaa equals stop translation

Query Match 99.8%; Score 607; DB 12; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Query Match 99.8%; Score 607; DB 12; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SDFCLGCAAAPPAPERLLWPILGGALSLTFFVLGLSGFLVWRRCRERSSPPP 113  
 Db 61 SDFCLGCAAAPPAPERLLWPILGGALSLTFFVLGLSGFLVWRRCRERSSPPP 113

RESULT 2  
 US-10-062-831-59  
 ; Sequence 59, Application US/10062831 -  
 ; Publication No. US20030105297A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Steven M. Ruben, et al.  
 ; TITLE OF INVENTION: 32 Human Secreted Proteins  
 ; FILE REFERENCE: P2006P1  
 ; CURRENT APPLICATION NUMBER: US/10/062, 831  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 09/690, 454  
 ; PRIOR FILING DATE: 1998-11-10  
 ; PRIOR APPLICATION NUMBER: PCT/US98/10868  
 ; PRIOR FILING DATE: May 28, 1998  
 ; PRIOR APPLICATION NUMBER: 60/044, 039  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048, 093  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048, 190  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/050, 935  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048, 101  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/048, 356  
 ; PRIOR FILING DATE: May 30, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056, 250  
 ; PRIOR FILING DATE: August 29, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056, 296  
 ; PRIOR FILING DATE: August 29, 1997  
 ; PRIOR APPLICATION NUMBER: 60/056, 293  
 ; PRIOR FILING DATE: August 29, 1997  
 ; NUMBER OF SEQ ID NOS: 229  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 59  
 ; LENGTH: 114  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (114)  
 ; OTHER INFORMATION: Xaa equals stop translation

Query Match 99.8%; Score 607; DB 15; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 QY 61 SDFCLGCAAAPPAPERLLWPILGGALSLTFFVLGLSGFLVWRRCRERSSPPP 113

RESULT 3  
 US-09-742-454-A-4  
 ; Sequence 4, Application US/09742454A  
 ; Patent No. US20020041876A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILEY, Steven R.  
 ; TITLE OF INVENTION: TWEAK Receptor  
 ; FILE REFERENCE: 2968-B  
 ; CURRENT APPLICATION NUMBER: US/09/742, 454A  
 ; CURRENT FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/172, 878  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: 60/203, 347  
 ; PRIOR FILING DATE: 2000-05-10  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 93.9%; Score 571; DB 9; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

RESULT 4  
 US-09-883-777-4  
 ; Sequence 4, Application US/09883777  
 ; Patent No. US20020110853A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILEY, Steven R.  
 ; TITLE OF INVENTION: TWEAK RECEPTOR  
 ; FILE REFERENCE: 2968-C  
 ; CURRENT APPLICATION NUMBER: US/09/883, 777  
 ; CURRENT FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: US 60/172, 878  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/203, 347  
 ; PRIOR FILING DATE: 2000-05-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/34755  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: US 09/742, 454  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 4  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens

Query Match 93.9%; Score 571; DB 10; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Query Match 99.8%; Score 607; DB 15; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-51;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 QY 61 SDFCLGCAAAPPAPERLLWPILGGALSLTFFVLGLSGFLVWRRCRERSSPPP 113

RESULT 5

Db 61 SDFCLGCAAAPPAPRLLWPILGALSITFVLRREKFTTP 113  
; Sequence 178, Application US/10024298A  
; Publication No. US20030143540A1

; GENERAL INFORMATION:

; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA  
; APPLICANT: Akio MATSUDA  
; APPLICANT: Goichi HONDA  
; APPLICANT: Shuji MURAMATSU  
; APPLICANT: Yukiko NAGANO

; TITLE OF INVENTION: NF-K B Activating Gene  
; FILE REFERENCE: 1254-0191P  
; CURRENT APPLICATION NUMBER: US/10/024,298A

; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/278,641  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP0088912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-024-298A-178

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVLGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
Db 1 MARGSLRRLRLLVLGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60

Qy 61 SDFCLGCAAAPPAPRLLWPILGALSITFVLRREKFTTP 113  
Db 61 SDFCLGCAAAPPAPRLLWPILGALSITFVLRREKFTTP 113

RESULT 6

US-10-042-211A-178  
; Sequence 178, Application US/10042211A  
; Publication No. US20030170719A1

; GENERAL INFORMATION:

; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFKB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-08912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 37  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-331-496A-37

Query Match 93.9%; Score 571; DB 12; Length 129;  
Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVLGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60  
Db 1 MARGSLRRLRLLVLGLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRARPH 60

QY 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113

GENERAL INFORMATION:  
 APPLICANT: Afar, Daniel  
 APPLICANT: Aziz, Natasha  
 APPLICANT: Ginsberg, Wendy M.  
 APPLICANT: Gish, Kurt C.  
 APPLICANT: Glynné, Richard  
 APPLICANT: Hevezí, Peter A.  
 APPLICANT: Mack, David H.  
 APPLICANT: Murray, Richard  
 APPLICANT: Watson, Susan R.

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-012500US

CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 60/356,714

PRIOR FILING DATE: 2002-02-13

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1386

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 444

LENGTH: 129

TYPE: PRT

ORGANISM: Homo sapiens

US-10-295-027-444

QY 93.9%; Score 571; DB 12; Length 129;  
 Best Local Similarity 94.7%; Pred. No. 5.7e-48;  
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gap

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 1 MARGSLRRLRLLWVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRA

QY 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRRERSSSPPP 113  
 Db 61 SDFCLGCAAAPPAPFRLWPILGGALSLTFLVGLLSGFLVWRRCRRERKFTTP 113

RESULT 9  
 US-10-295-027-1305  
 ; Sequence 1305, Application US/10295027  
 ; Publication No. US20030232350A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Afar, Daniel

;

LENGTH: 129  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 74.0%; Score 450; DB 9; Length 129;  
Best Local Similarity 75.2%; Pred. No. 3.2e-36;  
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60  
Db 1 MAPGWPRSLPQILVLGFLVLMRAAAGEQAPGTSPCSSSSWSADL DKCMDCA SCRAPH 60

Qy 61 SDFCLGCAAAPPAPFLLWPILGALSLTFLVGLLSGFLVWRRCRRERSSSPP 113  
Db 61 SDFCLGCAAAPPAPAHFRLLWPILGALSLVLA VSSFLVWRRCRRERKFTTP 113

RESULT 11  
US-09-883-777-5  
; Sequence 5, Application US/09883777  
; Patent No. US20020110853A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-883-777-5

Query Match 74.0%; Score 450; DB 10; Length 129;  
Best Local Similarity 75.2%; Pred. No. 3.2e-36;  
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

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Db 1 MAPGWPRSLPQILVLGFLVLMRAAAGEQAPGTSPCSSSSWSADL DKCMDCA SCRAPH 60

Qy 61 SDFCLGCAAAPPAPFLLWPILGALSLTFLVGLLSGFLVWRRCRRERSSSPP 113  
Db 61 SDFCLGCAAAPPAPAHFRLLWPILGALSLVLA VSSFLVWRRCRRERKFTTP 113

RESULT 12  
US-09-742-454A-7  
; Sequence 7, Application US/09742454A  
; Patent No. US20020041876A1  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0

Query Match 71.2%; Score 433; DB 9; Length 309;  
Best Local Similarity 74.1%; Pred. No. 3.5e-34;  
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

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Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60

Qy 61 SDFCLGCAAAPPAPFLLWPILGALSLTFLVGLLSGFLVWRRCRRERSSSPP 112  
Db 61 SDFCLGCAAAPPAPFLLWPILGALSLVLA VSSFLVWRRCRRERKFTTP 112

RESULT 13  
US-09-883-777-7  
; Sequence 7, Application US/09883777  
; Patent No. US20020110853A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7

Query Match 71.2%; Score 433; DB 10; Length 309;  
Best Local Similarity 74.1%; Pred. No. 3.5e-34;  
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

Qy 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60  
Db 1 MARGSLRRLRLVGLWALLRSVAGEQAPGTAPCSRGSWSADL DKCMDCA SCRAPH 60

Qy 61 SDFCLGCAAAPPAPFLLWPILGALSLTFLVGLLSGFLVWRRCRRERSSSPP 112  
Db 61 SDFCLGCAAAPPAPFLLWPILGALSLVLA VSSFLVWRRCRRERKFTTP 112

RESULT 14  
US-09-883-777-9  
; Sequence 9, Application US/09883777  
; Patent No. US20020110853A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18

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; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
; US-09-883-777-9

Query Match      62.4%;  Score 379.5;  DB 10;  Length 300;
Best Local Similarity 88.0%;  Pred. No. 5.2e-29;
Matches 73;  Conservative 0;  Mismatches 1;  Indels 9;  Gaps 1;

Qy          1 MARGSLRRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60
Db          1 MARGSLRRRLRLVGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

Qy          61 SDFCLGCAA-----PPAP 74
Db          61 SDFCLGCAAARSCKTHTCPPCP 83

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RESULT 15
US-10-251-947-4
; Sequence 4, Application US/10251947
; Publication No. US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-251-947-4

Query Match      16.0%;  Score 97.5;  DB 15;  Length 171;
Best Local Similarity 31.8%;  Pred. No. 0.069;
Matches 34;  Conservative 9;  Mismatches 39;  Indels 25;  Gaps 5;

Qy          23 RSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRAPHISDFCLGCAAAPPFRLLWP-- 80
Db          6 RSLRGRDAPVPTPCVPTECYDILVRKCVDCRLLRKSPPK---TAAGASSPAPGTALQPQE 62

Qy          81 -----ILGGA---LSLTFLVGL-LSGFLYMRRCRER 108
Db          63 SVGTGSGEVSLPLPGILLFGAPALLGLVVLVGLVSWRR-RQQR 108

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